

133817

STIC-Biotech/ChemLib

From: Schnizer, Holly
Sent: Tuesday, September 28, 2004 8:43 PM
To: STIC-Biotech/ChemLib
Subject: seq. search for appl. no. 10/049,399

Please search all databases for the following sequence:

residues 2169-2332 of SEQ ID NO:1

Thank you.

Holly Schnizer
AU 1653
Office: REM 3C79
Mailbox: REM 3C70
(571)272-0958

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: 9/29/04
Date Completed: 9/30/04
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA Sequence: # _____
AA Sequence: # 1
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: Q2P
WWW/Internet: _____
Other(Specify): _____

This Page Blank (uspto)

Result No.	Query %		DB	ID	Description
	Score	Match Length			
1	871	100.0	6	ABP60514	Abp60514 Human fac
2	871	100.0	684	ABP73022	Abp73022 Human fac
3	871	100.0	684	AAR74091	Aar74091 Factor-VI
4	871	100.0	790	AD654594	Ad654594 Recombina
5	871	100.0	1014	APF71139	Apf71139 Factor VII
6	871	100.0	1383	AAW333227	Aaw333227 Procoagul
7	871	100.0	1383	AAW333228	Aaw333228 Procoagul
8	871	100.0	1383	AAR333229	Aar333229 Procoagul
9	871	100.0	1424	AAE80268	Aae80268 Modified
10	871	100.0	1424	APF91169	Apf91169 Sequence
11	871	100.0	1424	AAB48842	Aab48842 Mutant ma
12	871	100.0	1424	AAO18692	Aao18692 Human mat
13	871	100.0	1425	AAE90267	Aae90267 Modified
14	871	100.0	1438	AAE01282	Aae01282 B-domain
15	871	100.0	1440	AAR12971	Aar12971 Factor VI
16	871	100.0	1445	ABG92540	Abg92540 LE B-doma
17	871	100.0	1447	ABG92541	Abg92541 SArg B-do
18	871	100.0	1457	AAW46246	Aaw46246 Human fac
19	871	100.0	1457	AAW44372	Aaw44372 Human fac
20	871	100.0	1457	AAAY21675	Aay21675 Beta-doma
21	871	100.0	1459	AAE10832	Aae10832 Human fac
22	871	100.0	1471	AAW23414	Aaw23414 Human B-d
23	871	100.0	1471	AAAB67959	Aab67959 Amino aci
24	871	100.0	1516	AAE80265	Aae80265 Modified
25	871	100.0	1661	AAW18570	Aaw18570 Factor VI

The invention relates to a novel recombinant modified functional polypeptide which exerts at least one function of a mammalian protein and which eliminates or reduces by at least about 80% with respect to activation by the unmodified polypeptide, the activation of at least one T-cell clone derived from a mammal with antibody against the unmodified polypeptide. The polypeptide of the invention has haemostatic activity. The polynucleotide encoding the polypeptide may have a use in gene therapy. The recombinant modified functional polypeptide is useful as a medicament for treating or preventing a thrombotic disorder, such as haemophilia A or B. The peptide is also useful for *in vitro* or *in vivo* evaluation and/or modulation of T-cell reactivity. The recombinant point-

CC mutated factor VIII light chain molecule is used as a template for
 CC determining whether modification of the factor VIII molecule is able to
 CC reduce the clearance, e.g. to increase the half-time, of factor VIII in
 CC plasma. The present sequence represents the human factor VIII light chain
 CC P2153Q mutant
 CC XX
 CC SQ

Sequence 643 AA;

Query Match 100.0%; Score 871; DB 6; Length 643;
 Best Local Similarity 100.0%; Pred. No. 2.9e-90;
 Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDLNSCSMPLGMSKALSDAQITASSYFTNMFTWSPSKARHLQGRSNARWPQVNNPKE 60
 DB 480 CDLNSCSMPLGMSKALSDAQITASSYFTNMFTWSPSKARHLQGRSNARWPQVNNPKE 539
 QY 61 WLQVDFQKTMKVGTGGVTKGKSLTSMYKVEFLISSQDGHQWTLFFQNGKVKVFGNQD 120
 DB 540 WLQVDFQKTMKVGTGGVTKGKSLTSMYKVEFLISSQDGHQWTLFFQNGKVKVFGNQD 599
 QY 121 SFTFVNSLDPPLTLRLRHPSQVHQAIALRMEVLGCEAQDLY 164
 DB 600 SFTFVNSLDPPLTLRLRHPSQVHQAIALRMEVLGCEAQDLY 643

RESULT 2
 AAR73022
 ID AAR73022 standard; peptide; 684 AA.

XX AAR73022;
 XX 25-MAR-2003 (revised)
 DT 21-NOV-1995 (first entry)
 XX
 XX Human Factor-VIII C-terminal fragment.

XX Factor-VIII; blood-clotting; blood; coagulant; haemophilia-A.

XX Homo sapiens.

XX WO9513301-A1.

XX 18-MAY-1995.

XX 10-NOV-1994; 94WO-DK000424.

XX 12-NOV-1993; 93DK-00001281.

XX (NOVO) NOVO-NORDISK AS.

XX Persson E;

XX WPI; 1995-194038/25.

XX Crosslinked Factor VIII polypeptide which is stable - is prepnd. using
 PT bis(sulphosuccinimidy)l suberate or disuccinimidy)l suberate in the
 PT presence of polysorbate 80 to produce a coagulant with long lasting
 PT activity.

XX Disclosure; Page 24; 36pp; English.

XX This is the C-terminal fragment (corresponding to AAs 1649-2332) of human
 CC Factor-VIII which may be crosslinked resulting in increased stability and
 CC retention of high activity over extended periods of time after activation
 CC by thrombin. The polypeptide is used to prevent or treat diseases caused
 CC by the absence or deficiency of Factor-VIII in a subject such as
 CC haemophilia. (Updated on 25-MAR-2003 to correct PN field.)
 CC XX

SQ Sequence 684 AA;

Query Match 100.0%; Score 871; DB 2; Length 684;
 Best Local Similarity 100.0%; Pred. No. 3.2e-90;
 Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDLNSCSMPLGMSKALSDAQITASSYFTNMFTWSPSKARHLQGRSNARWPQVNNPKE 60
 DB 521 CDLNSCSMPLGMSKALSDAQITASSYFTNMFTWSPSKARHLQGRSNARWPQVNNPKE 580
 QY 61 WLQVDFQKTMKVGTGGVTKGKSLTSMYKVEFLISSQDGHQWTLFFQNGKVKVFGNQD 120
 DB 581 WLQVDFQKTMKVGTGGVTKGKSLTSMYKVEFLISSQDGHQWTLFFQNGKVKVFGNQD 640
 QY 121 SFTFVNSLDPPLTLRLRHPSQVHQAIALRMEVLGCEAQDLY 164
 DB 641 SFTFVNSLDPPLTLRLRHPSQVHQAIALRMEVLGCEAQDLY 684

RESULT 3

AAR74091
 ID AAR74091 standard; protein; 684 AA.

XX AAR74091;

XX 25-MAR-2003 (revised)

DT 04-NOV-1995 (first entry)

XX Factor-VIII light chain C-terminal fragment.

XX human; Factor VIII; light chain; C-terminal fragment; thrombin cleavage;
 KW blood-clotting.

XX Homo sapiens.

XX WO9513300-A1.

XX 18-MAY-1995.

XX 10-NOV-1994; 94WO-DK000423.

XX 12-NOV-1993; 93DK-00001280.

XX (NOVO) NOVO-NORDISK AS.

XX Kjalke M, Ezban Rasmussen M;

XX WPI; 1995-194037/25.

XX Factor VIII polypeptide(s) comprising a heavy chain shorter than native
 PT A1-A2 domain - are easier to produce recombinantly and retain coagulant
 PT activity, may be used to treat patients who have developed antibodies to
 PT C-terminal epitope(s) of Factor VIII.

XX Claim 4; Page 33-35; 51pp; English.

XX The sequence represents C-terminal residues 1649-2332 of a human Factor-
 CC VIII light chain. The sequence is produced by treating a full-length
 CC Factor-VIII polypeptide with a protease, e.g. thrombin. The fragment may
 CC be produced recombinantly in conjunction with a C-terminally truncated
 CC heavy chain to reduce production costs and improve safety, and production
 CC levels and stability are higher than for the full-length form. When the
 CC fragment is used along with a C-terminally truncated heavy chain, it may
 CC be used to treat patients who have developed antibodies against epitopes
 CC in the C-terminal part of the heavy chain. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 CC XX

SQ Sequence 684 AA;

Query Match 100.0%; Score 871; DB 2; Length 684;
 Best Local Similarity 100.0%; Pred. No. 3.2e-90;
 Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDLNSCSMPLGMSKALSDAQITASSYFTNMFTWSPSKARHLQGRSNARWPQVNNPKE 60
 DB 521 CDLNSCSMPLGMSKALSDAQITASSYFTNMFTWSPSKARHLQGRSNARWPQVNNPKE 580
 QY 61 WLQVDFQKTMKVGTGGVTKGKSLTSMYKVEFLISSQDGHQWTLFFQNGKVKVFGNQD 120

Db 581 WLQVDFQKMTKVTGTTQGVKSLTSMYKFLISSQDGHQWTLFFQNGKVKVFGNQD 640
 QY 121 SFTPVVNSLDPPLRLRYLRHPQSWVHQIALRMEVLGCEAODLY 164
 Db 641 SFTPVVNSLDPPLRLRYLRHPQSWVHQIALRMEVLGCEAODLY 684

RESULT 4
 ADE64594
 ID ADE64594 standard; protein; 790 AA.
 AC ADE64594;
 XX
 XX 29-JAN-2004 (first entry)
 DT
 DE Recombinant blood coagulation factor VIII protein, SEQ ID 4.
 XX
 XX blood coagulation factor VIII; type-A haemophilia.
 KW
 KW Unidentified.
 OS
 XX CN1361178-A.
 PN
 XX 31-JUL-2002.
 PD
 XX 29-DEC-2000; 2000CN-00137779.
 PF
 XX 29-DEC-2000; 2000CN-00137779.
 PR
 XX (SHAN-) SHANGHAI BIO-CHEM INST CHINESE ACAD SCI.
 PA
 XX Qi Z, Wang Q, Chen C;
 PI WPI; 2002-741852/81.
 DR N-PSDB; ADE64593.
 XX
 XX New recombinant blood coagulation factor VIII and its production process
 PT and medicinal composition.
 PT
 XX Claim 2; SEQ ID NO 4; 31pp; Chinese.
 PS
 XX The invention relates to a novel recombinant blood coagulation factor
 CC VIII, its production process and its medicinal composite for treating
 CC type-A haemophilia. The invention further comprises a medicinal
 CC composition containing the blood coagulation factor which promotes blood
 CC coagulation to the blood plasma of type-A haemophilia patients. This
 CC sequence represents a recombinant blood coagulation factor VIII protein
 CC of the invention.
 CC
 XX
 SQ Sequence 790 AA;

Query Match 100.0%; Score 871; DB 5; Length 790;
 Best Local Similarity 100.0%; Pred. No. 3.9e-90;
 Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDLNSCSMPLGWSKASDAQITASSYFTNNFATWSPSKARLHLQGRSNARVQVNNPKE 60
 Db 627 CDLNSCSMPLGWSKASDAQITASSYFTNNFATWSPSKARLHLQGRSNARVQVNNPKE 686
 QY 61 WLQVDFQKMTKVTGTTQGVKSLTSMYKFLISSQDGHQWTLFFQNGKVKVFGNQD 120
 Db 687 WLQVDFQKMTKVTGTTQGVKSLTSMYKFLISSQDGHQWTLFFQNGKVKVFGNQD 746
 QY 121 SFTPVVNSLDPPLRLRYLRHPQSWVHQIALRMEVLGCEAODLY 164
 Db 747 SFTPVVNSLDPPLRLRYLRHPQSWVHQIALRMEVLGCEAODLY 790

RESULT 5
 AAP71139
 ID AAP71139 standard; protein; 1014 AA.
 XX

AC AAP71139;
 XX 25-MAR-2003 (revised)
 DT 14-MAY-1991 (first entry)
 XX
 DE Factor VIII:c variant.
 XX
 KW Factor VIII:c; variant; proteolysis; resistance;
 KW pro coagulation activity.
 XX
 OS Homo sapiens.
 PN W08707144-A.
 XX
 PD 03-DEC-1987.
 XX
 PF 29-MAY-1987; 87WO-US001299.
 XX
 PR 29-MAY-1986; 86US-00868410.
 PR 18-NOV-1986; 86US-00932767.
 PR 09-DEC-1986; 86US-00939658.
 XX
 XX (GEMY) GENETICS INST INC.
 PA
 XX Kaufman RJ, Pittman D, Toole JJ;
 PI WPI; 1987-348539/49.
 DR
 XX New deletion and replacement variants of factor 8:c - resistant to
 PT proteolysis but retaining pro-coagulant activity, and new DNA coding
 PT sequences.
 PS
 XX Disclosure; Page 1; 42pp; English.
 XX
 CC The full-length human factor VIII:c cDNA has been set forth in detail in
 CC W08501961. This sequence is an example of the formula A-X-B, wherein
 CC A-Ala1-Arg372, B-Ser1690-Tyr2332 and X=0-1316 amino acids substantially
 CC duplicative of sequences of amino acids within the sequence Arg372-
 CC Ser1690 of the full-length sequence. Here X=0; producing a Arg371-Ser1690
 CC fusion protein. One or more deletions or replacements at Arg 220, 226,
 CC 279, 282, 336, 359, 1719, 1721 and Lys 325, 338 and Tyr 346 will produce
 CC variants which are more resistant to specific proteolytic cleavage
 CC compared with natural factor VIII:c. Pro-coagulant activity and thrombin
 CC activatability have been retained. See also AAP711726-29. (Updated on 25-
 CC MAR-2003 to correct PA field.)
 XX
 SQ Sequence 1014 AA;

Query Match 100.0%; Score 871; DB 1; Length 1014;
 Best Local Similarity 100.0%; Pred. No. 5.5e-90;
 Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDLNSCSMPLGWSKASDAQITASSYFTNNFATWSPSKARLHLQGRSNARVQVNNPKE 60
 Db 851 CDLNSCSMPLGWSKASDAQITASSYFTNNFATWSPSKARLHLQGRSNARVQVNNPKE 910
 QY 61 WLQVDFQKMTKVTGTTQGVKSLTSMYKFLISSQDGHQWTLFFQNGKVKVFGNQD 120
 Db 911 WLQVDFQKMTKVTGTTQGVKSLTSMYKFLISSQDGHQWTLFFQNGKVKVFGNQD 970
 QY 121 SFTPVVNSLDPPLRLRYLRHPQSWVHQIALRMEVLGCEAODLY 164
 Db 971 SFTPVVNSLDPPLRLRYLRHPQSWVHQIALRMEVLGCEAODLY 1014

RESULT 6
 AAW33227
 ID AAW33227 standard; protein; 1383 AA.
 XX
 XX AAW33227;
 XX
 XX 30-APR-1998 (first entry)
 XX

XX PD 30-OCT-1997.
 XX XX
 XX PF 24-APR-1997; 97WO-US006563.
 XX XX
 PR 24-APR-1996; 96US-0016117P.
 PR 15-MAY-1996; 96US-0017785P.
 XX XX
 PA (UNMI) UNIV MICHIGAN.
 XX XX
 XX Kaufman RJ, Pipe SW, Amano K;
 PI WPI; 1997-535830/49.
 XX DR
 XX PT Modified human pro-coagulant active factor VIII - can be administered to
 PT haemophiliacs, i.e. factor VIII replacement therapy.
 XX XX
 XX PS Claim 19; Page; 57pp; English.
 XX CC
 CC The present sequence represents a novel pro-coagulant active factor VIII
 CC (FVIII) mutant protein, comprising a deletion of the B domain and von
 CC Willebrand factor binding site, mutations F309S, R740A and addition of an
 CC amino acid sequence spacer between the A2 and A3 domains. Factor VIII,
 CC along with calcium and phospholipid, acts as a cofactor for factor IXA,
 CC when it converts factor X to the activated form (factor Xa). FVIII is the
 CC coagulation factor deficient in the X-chromosome-linked bleeding disorder
 CC haemophilia A. Several other mutant FVIII proteins have also been created
 CC (see AAW33222-29). The FVIII mutant F309S (AAW33225) is capable of
 CC recombinant secretion at higher levels than typically obtained with wild
 CC type FVIII and retains pro-coagulant activity. The FVIII mutant R336I
 CC (AAW33222) and R562K (AAW33223) are resistant to activated protein C
 CC (APC) cleavage. The present FVIII mutant can form a more stable
 CC configuration, and have an approximate 5-fold increase in specific
 CC activity compared to purified wild type FVIII, while increasing their
 CC binding affinity to von Willebrand factor improves their stability. The
 CC FVIII proteins can be administered to haemophiliacs, i.e. FVIII
 CC replacement therapy, while the nucleic acid molecule can be used for gene
 CC therapy. note: this sequence does not appear in the specification; it was
 CC created using sequences from the given references
 XX XX
 SQ Sequence 1383 AA;
 Query Match 100.0%; Score 871; DB 2; Length 1383;
 Best Local Similarity 100.0%; Pred. No. 8.6e-90;
 Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CDLNSCMPLGMEKSAISDAQITASSYFTNMFATWSPSKARLHLOGRSNARFPQVNNPKE 60
 DB 1220 CDLNSCMPLGMEKSAISDAQITASSYFTNMFATWSPSKARLHLOGRSNARFPQVNNPKE 1279
 QY 61 WLQVDFQKTKMVTGVTGQVKSLLTSMYKFLISSQDGHQWTLFFQNGKVKVFGNQD 120
 DB 1280 WLQVDFQKTKMVTGVTGQVKSLLTSMYKFLISSQDGHQWTLFFQNGKVKVFGNQD 1339
 QY 121 SFTPVNSLDPPLLTRYLRHPQSWHQIALRMEVLGCEAQDLY 164
 DB 1340 SFTPVNSLDPPLLTRYLRHPQSWHQIALRMEVLGCEAQDLY 1383
 RESULT 9
 AAP80268
 ID AAP80268 standard; protein; 1424 AA.
 XX AC AAP80268;
 XX XX
 XX 25-MAR-2003 (revised)
 DT 10-OCT-1990 (first entry)
 XX XX
 DE Modified factor VIII:C sequence with the R740-D1658 deletion.
 XX Modified factor VIII:C; maturation polypeptide; haemophilia;
 XX blood coagulation; RD deletion; procoagulant.
 XX XX

OS Homo sapiens.
 XX XX
 EN WO8800831-A.
 XX XX
 PD 11-FEB-1988.
 XX XX
 PF 31-JUL-1987; 87WO-US001814.
 XX XX
 PR 01-AUG-1986; 86US-00893375.
 XX XX
 PA (BIOJ) BIOGEN NV.
 PA (PASE/) PASEK M P.
 XX XX
 PI Pasek MP;
 XX XX
 DR WPI; 1988-049866/07.
 DR N-PSDB; AAN80447.
 XX XX
 PT New DNA sequences encoding modified factor VIII:C - with deletion of DNA
 PT encoding maturation polypeptide, useful for high yield transformation.
 XX XX
 PS Claim 3; Page 60-61-62-63; 97pp; English.
 CC CC
 CC The RD deletion removes the DNA from Ser 741 to Ser 1657. A major part of
 CC the sequence encoding the maturation polypeptide of factor VIII:C is
 CC deleted, i.e. Gln 744 - Asp 1563. The full length Factor VIII:C cDNA has
 CC two changes with respect to the published sequence (BPO application
 CC 160457): CTG to CTA at Leu 242 and TTC to CTC change at amino acid
 CC residue 1880 (Phe to Leu). The product is produced in approx. 20 times
 CC higher yields than previous recombinant produced factor VIII:C and are
 CC more easily purified. The peptide is used for treating haemophilia A,
 CC both acute and prolonged bleeding. See also AAN80444 and AAN80446.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX XX
 SQ Sequence 1424 AA;
 Query Match 100.0%; Score 871; DB 1; Length 1424;
 Best Local Similarity 100.0%; Pred. No. 9e-90;
 Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CDLNSCMPLGMEKSAISDAQITASSYFTNMFATWSPSKARLHLOGRSNARFPQVNNPKE 60
 DB 1261 CDLNSCMPLGMEKSAISDAQITASSYFTNMFATWSPSKARLHLOGRSNARFPQVNNPKE 1320
 QY 61 WLQVDFQKTKMVTGVTGQVKSLLTSMYKFLISSQDGHQWTLFFQNGKVKVFGNQD 120
 DB 1321 WLQVDFQKTKMVTGVTGQVKSLLTSMYKFLISSQDGHQWTLFFQNGKVKVFGNQD 1380
 QY 121 SFTPVNSLDPPLLTRYLRHPQSWHQIALRMEVLGCEAQDLY 164
 DB 1381 SFTPVNSLDPPLLTRYLRHPQSWHQIALRMEVLGCEAQDLY 1424
 RESULT 10
 AAP91169
 ID AAP91169 standard; protein; 1424 AA.
 XX AC AAP91169;
 XX XX
 XX 25-MAR-2003 (revised)
 DT 26-JUN-1990 (first entry)
 XX XX
 DE Sequence of 740 Arg-1649 Glu human Factor VIII:C.
 XX Human Factor VIII:C; Ad.RE.neo; 740 Arg-1649 Glu Factor VIII:C;
 XX haemophilia A.
 XX Homo sapiens.
 OS Homo sapiens.
 XX EF306968-A.
 XX XX
 XX 15-MAR-1989.
 XX XX

PF 09-SEP-1988; 88EP-00114769.
 XX
 PR 10-SEP-1987; 87JP-00225147.
 PR 08-APR-1988; 88JP-00085454.
 XX
 PA (KAGA) CHEMO SERO THERAPEUTIC RES INST.
 PA (TEIJU) TEIJUN LTD.
 XX
 PI Sugiyama T, Masuda K, Tajima Y, Yonemura H;
 XX WPI: 1989-078467/11.
 DR N-PSDB; AAN90654.
 DR
 XX Prodn. of recombinant human Factor-VIII-C - using animal cells
 PT transformed with a vector contg. the gene for Factor VIII:C and a
 PT promoter.
 PT
 XX
 PS Disclosure; Fig 1; 32pp; English.
 XX
 CC Arg-740 of the carboxyl terminus of the H chain is directly bonded by a
 CC peptide bond to Glu-1649 of the amino terminus of L chain. A prefd.
 CC expression vector used to transform animal cell so that they produce
 CC human Factor VIII:Cis plasmid Ad.RE.neo. The expression vector has at
 CC least one promoter upstream of AAN90654. The transformants can constantly
 CC and continuously produce human Factor VIII:C in high yield on a
 CC commercial scale. The human Factor VIII:C so produced is considered to
 CC corresp. to the smallest species of active and intact Factor VIII:C
 CC molecules in the human blood plasma. It is useful for treating
 CC haemophilia A patients. (Updated on 25-MAR-2003 to correct PR field.)
 CC (Updated on 25-MAR-2003 to correct PA field.)
 CC
 XX SQ Sequence 1424 AA;

Query Match 100.0%; Score 871; DB 1; Length 1424;
 Best Local Similarity 100.0%; Pred. No. 9e-90;
 Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDLNSCSMPGLGMSKAISSDAQITASSYFTNMFTWSPSKARLHLQGRSNARWPQVNNPKE 60
 DB 1261 CDLNSCSMPGLGMSKAISSDAQITASSYFTNMFTWSPSKARLHLQGRSNARWPQVNNPKE 1320

QY 61 WLQVDFQKTMKVTGVTGQVKSLTSMYKFEFLISSQDGHQWTLFFQNGKVKVFGNQD 120
 DB 1321 WLQVDFQKTMKVTGVTGQVKSLTSMYKFEFLISSQDGHQWTLFFQNGKVKVFGNQD 1380

QY 121 SFTPVNSLDPPLLTRYLRIHPQSWVHQIALRMEVLGCEAQDLY 164
 DB 1381 SFTPVNSLDPPLLTRYLRIHPQSWVHQIALRMEVLGCEAQDLY 1424

RESULT 11
 AAB48842
 ID AAB48842 standard; protein; 1424 AA.
 XX
 AC AAB48842;
 XX
 DT 13-MAR-2001 (first entry)
 XX
 DE Mutant mature human factor VIII, SEQ ID NO:5.
 XX
 KW Factor VIII; human; B domain; LRP-mediated plasma clearance;
 KW receptor-dependent clearance; receptor-independent clearance; half-life;
 KW haemophilia; mutant; mutein.
 XX
 OS Homo sapiens.
 XX
 PN WO200071714-A2.
 XX
 XX 30-NOV-2000.
 XX
 XX 24-MAY-2000; 2000WO-US014111.
 XX
 XX 24-MAY-1999; 99US-0135847P.
 PR

XX (AMNA-) AMERICAN NAT RED CROSS.
 PA
 XX Saenko EL, Strickland DK;
 PI
 XX WPI: 2001-025163/03.
 DR
 XX Factor VIII mutants having increased half-life useful for treating
 FT hemophilia, comprise one or more amino acid substitutions in the A2
 FT and/or C2 domain of factor VIII.
 FT
 XX Claim 9; Fig 2A-B; 121pp; English.
 PS
 XX The invention relates to human factor VIII mutants comprising an amino
 CC acid substitution at one or more positions in the A2 domain and/or an
 CC amino acid substitution at one or more positions in the C2 domain. The
 CC invention also encompasses a factor VIII mutant which lacks a B domain
 CC (AAB48842). The factor VIII mutants have an increased half-life in the
 CC bloodstream. The A2 domain mutants exhibit increased LRP-dependent
 CC (receptor-dependent) clearance of factor VIII, while C2 domain mutants
 CC have reduced receptor-independent clearance. The invention also relates
 CC to a method of using RAP (receptor associated protein), a protein which
 CC inhibits LRP (low density lipoprotein related protein), mediated ligand
 CC internalisation, to increase the half-life of factor VIII. The mutant
 CC factor VIII proteins, and nucleotides encoding them, are useful for
 CC treating haemophilia. RAP, LRP-binding RAP mutants or fragments, and
 CC nucleic acids encoding them may also be used in the treatment of
 CC haemophilia, in combination with a mutant factor VIII protein or DNA of
 CC the invention. The invention provides means of increasing the half-life
 CC of factor VIII by reducing its clearance from plasma. The present
 CC sequence represents a mutant mature human factor VIII which lacks a B
 CC domain
 XX SQ Sequence 1424 AA;

Query Match 100.0%; Score 871; DB 4; Length 1424;
 Best Local Similarity 100.0%; Pred. No. 9e-90;
 Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDLNSCSMPGLGMSKAISSDAQITASSYFTNMFTWSPSKARLHLQGRSNARWPQVNNPKE 60
 DB 1261 CDLNSCSMPGLGMSKAISSDAQITASSYFTNMFTWSPSKARLHLQGRSNARWPQVNNPKE 1320

QY 61 WLQVDFQKTMKVTGVTGQVKSLTSMYKFEFLISSQDGHQWTLFFQNGKVKVFGNQD 120
 DB 1321 WLQVDFQKTMKVTGVTGQVKSLTSMYKFEFLISSQDGHQWTLFFQNGKVKVFGNQD 1380

QY 121 SFTPVNSLDPPLLTRYLRIHPQSWVHQIALRMEVLGCEAQDLY 164
 DB 1381 SFTPVNSLDPPLLTRYLRIHPQSWVHQIALRMEVLGCEAQDLY 1424

RESULT 12
 AAO18622
 ID AAO18622 standard; protein; 1424 AA.
 XX
 AC AAO18622;
 XX
 DT 24-OCT-2002 (first entry)
 XX
 DE Human mature B-domainless factor VIII.
 XX
 KW Human; factor VIII; fvIII; half-life; mutant; haemophilia;
 KW heparan sulfate proteoglycan-mediated clearance; RAP;
 KW receptor-associated protein; haemostatic; gene therapy;
 KW alpha2 macroglobulin receptor-associated protein.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH 373..740
 FT Domain /label= A2_domain
 FT 484..509
 FT Region

FT XX /label= LRP_binding_region
 XX WO200260951-A2.
 XX 08-AUG-2002.
 XX
 XX 11-JAN-2002; 2002WO-US000583.
 XX
 XX 12-JAN-2001; 2001US-0250904P.
 XX (AMNA-) AMERICAN NAT RED CROSS.
 XX
 XX Saenko EL, Sarafanov AG;
 XX WPI; 2002-608501/65.
 XX
 XX New mutant factor VIII with reduced sulfate proteoglycan (HSPG)-dependent
 XX or receptor-independent clearance and procoagulant activity for treating
 XX hemophilia.
 XX
 XX Claim 9; Fig 12; 151pp; English.
 XX
 XX The present invention relates to a mutant factor VIII protein with
 XX reduced sulfate proteoglycan (HSPG)-dependent or receptor-independent
 XX clearance and procoagulant activity, which has a nonconservative amino
 XX acid substitution at one or more positions in the A2 domain consisting of
 XX Lys(380, 512, 556, 570 or 659) or Arg(490, 527, 562 or 571) or in the C2
 XX domain relative to the wild-type. The mutant factor VIII or the
 XX polynucleotide encoding it and a receptor-associated protein (alpha2
 XX macroglobulin receptor-associated protein or RAP) are useful for treating
 XX haemophilia. The mutated protein has a longer half-life. The present
 XX sequence is the human mature B-domainless factor VIII protein
 XX
 XX SQ Sequence 1424 AA;
 XX
 XX Query Match 100.0%; Score 871; DB 5; Length 1424;
 XX Best Local Similarity 100.0%; Pred. No. 9e-90;
 XX Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 CDLNSCSMPLGMSKALSDAQITASSYFTNMFTWSPSKARLHLQGRSNARWPQVNNPKE 60
 XX Db 1261 CDLNSCSMPLGMSKALSDAQITASSYFTNMFTWSPSKARLHLQGRSNARWPQVNNPKE 1320
 XX
 XX QY 61 WLQVDFQKTMKVGTGGVTTQGVKSLTSMYKVEFLISSQDGHQWTLFFQNGKVKVFGNQD 120
 XX Db 1321 WLQVDFQKTMKVGTGGVTTQGVKSLTSMYKVEFLISSQDGHQWTLFFQNGKVKVFGNQD 1380
 XX
 XX QY 121 SFTPVVNSLDPPLLTLYRLRHPSQSWHQAIALRMEVLGCEAQDLY 164
 XX Db 1381 SFTPVVNSLDPPLLTLYRLRHPSQSWHQAIALRMEVLGCEAQDLY 1424
 XX
 XX RESULT 13
 XX AAP80267
 XX ID AAP80267 standard; protein; 1425 AA.
 XX AC AAP80267;
 XX
 XX DT 25-MAR-2003 (revised)
 XX DT 10-OCT-1990 (first entry)
 XX
 XX DE Modified factor VIII:C sequence with the R740-E1649 deletion.
 XX
 XX KW Modified factor VIII:C; maturation polypeptide; haemophilia;
 XX KW blood coagulation; RE deletion.
 XX
 XX OS Homo sapiens.
 XX
 XX PN WO8800831-A.
 XX PD 11-FEB-1988.
 XX
 XX PF 31-JUL-1987; 87WO-US001814.

XX
 XX PR 01-AUG-1986; 86US-008933375.
 XX
 XX PA (BIOJ) BIOGEN NV.
 XX PA (PASE/) PASEK M P.
 XX
 XX PI Pasek MP;
 XX
 XX DR WPI; 1988-049866/07.
 XX DR N-PSDB; AAN80446.
 XX
 XX PT New DNA sequences encoding modified factor VIII:C - with deletion of DNA
 XX PT encoding maturation polypeptide, useful for high yield transformation.
 XX
 XX PS Claim 3; Page 57-58-59-60; 97pp; English.
 XX
 XX CC The entire sequence encoding the maturation polypeptide of factor VIII:C
 XX CC is deleted, i.e. Arg 740-Glu 1649. The full length factor VIII:C cDNA has
 XX CC two changes with respect to the published sequence (BPO application
 XX CC 160457): CTG to CTA at Leu 242 and TTC to CTC change at amino acid
 XX CC residue 1880 (Phe to Leu). The product is produced in approx. 20 times
 XX CC higher yields than previous recombinant produced factor VIII:C and are
 XX CC more easily purified. The peptide is used for treating haemophilia A,
 XX CC both acute and prolonged bleeding. See also AAN80444 and AAN80447.
 XX CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 XX SQ Sequence 1425 AA;
 XX
 XX Query Match 100.0%; Score 871; DB 1; Length 1425;
 XX Best Local Similarity 100.0%; Pred. No. 9e-90;
 XX Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 CDLNSCSMPLGMSKALSDAQITASSYFTNMFTWSPSKARLHLQGRSNARWPQVNNPKE 60
 XX Db 1262 CDLNSCSMPLGMSKALSDAQITASSYFTNMFTWSPSKARLHLQGRSNARWPQVNNPKE 1321
 XX
 XX QY 61 WLQVDFQKTMKVGTGGVTTQGVKSLTSMYKVEFLISSQDGHQWTLFFQNGKVKVFGNQD 120
 XX Db 1322 WLQVDFQKTMKVGTGGVTTQGVKSLTSMYKVEFLISSQDGHQWTLFFQNGKVKVFGNQD 1381
 XX
 XX QY 121 SFTPVVNSLDPPLLTLYRLRHPSQSWHQAIALRMEVLGCEAQDLY 164
 XX Db 1382 SFTPVVNSLDPPLLTLYRLRHPSQSWHQAIALRMEVLGCEAQDLY 1425
 XX
 XX RESULT 14
 XX AAB01262
 XX ID AAB01262 standard; protein; 1438 AA.
 XX AC AAB01262;
 XX
 XX DT 25-SEP-2000 (first entry)
 XX
 XX DE B-domain deleted factor VIII sequence.
 XX
 XX KW Factor VIII; procoagulant; adenovirus; adeno-associated strain;
 XX KW Gene therapy; human Burkitt's lymphoma; HKB; therapy;
 XX KW therapeutic protein; vector; Epstein-Barr virus; human.
 XX
 XX OS Homo sapiens.
 XX
 XX PN WO200034505-A1.
 XX PD 15-JUN-2000.
 XX
 XX PF 08-DEC-1999; 99WO-US029169.
 XX
 XX PR 10-DEC-1998; 98US-00209916.
 XX PA (FARB) BAYER CORP.
 XX
 XX PI Cho M, Chan SY, Kelsey W, Yee H;
 XX

```

Search completed: September 29, 2004, 16:38:58
Job time : 58 secs

```

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 29, 2004, 16:40:09 ; Search time 131 Seconds
(without alignments)
402.863 Million cell updates/sec

Title: US-10-049-399a-1_COPY_2169_2332

Perfect score: 871
Sequence: 1 CDLNSCSMPLGMSKAISDA.....VWQIALRNEVLGCEAQDLY 164

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/prodata/2/pubpaa/US07_PUBCOMB.pep:
2: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep:
3: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pep:
4: /cgn2_6/prodata/2/pubpaa/US06_PUBCOMB.pep:
5: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep:
6: /cgn2_6/prodata/2/pubpaa/PCTUS_PUBCOMB.pep:
7: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pep:
8: /cgn2_6/prodata/2/pubpaa/US08_PUBCOMB.pep:
9: /cgn2_6/prodata/2/pubpaa/US09_PUBCOMB.pep:
10: /cgn2_6/prodata/2/pubpaa/US09_PUBCOMB.pep:
11: /cgn2_6/prodata/2/pubpaa/US09C_PUBCOMB.pep:
12: /cgn2_6/prodata/2/pubpaa/US09_NEW_PUB.pep:
13: /cgn2_6/prodata/2/pubpaa/US10A_PUBCOMB.pep:
14: /cgn2_6/prodata/2/pubpaa/US10B_PUBCOMB.pep:
15: /cgn2_6/prodata/2/pubpaa/US10C_PUBCOMB.pep:
16: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pep:
17: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pep:
18: /cgn2_6/prodata/2/pubpaa/US60_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	871	100.0	1438	13	US-10-006-091-1
2	871	100.0	1438	13	US-10-047-257-1
3	871	100.0	1438	14	US-10-225-900-1
4	871	100.0	1459	16	US-10-239-498A-13
5	871	100.0	1471	12	US-10-681-970-2
6	871	100.0	1471	13	US-10-095-718-2
7	871	100.0	2332	9	US-09-957-641-2
8	871	100.0	2332	14	US-10-187-319-2
9	871	100.0	2332	14	US-10-131-510A-2
10	871	100.0	2332	15	US-10-445-235-2
11	871	100.0	2332	15	US-10-360-101-229
12	871	100.0	2332	16	US-10-239-498A-2
13	871	100.0	2332	16	US-10-466-998A-1
14	871	100.0	2351	12	US-10-411-037-30
15	871	100.0	2351	12	US-10-411-026-30

16	871	100.0	2351	14	US-10-132-829-4	Sequence 4, Appli
17	871	100.0	2351	14	US-10-172-712-27	Sequence 27, Appl
18	871	100.0	2351	14	US-10-133-907-4	Sequence 4, Appli
19	871	100.0	2351	16	US-10-410-962-30	Sequence 30, Appl
20	871	100.0	2351	16	US-10-411-049-30	Sequence 30, Appl
21	871	100.0	2351	16	US-10-410-930-30	Sequence 30, Appl
22	871	100.0	2351	16	US-10-410-997-30	Sequence 30, Appl
23	871	100.0	2351	16	US-10-411-012-30	Sequence 30, Appl
24	871	100.0	2351	16	US-10-287-994-30	Sequence 30, Appl
25	871	100.0	2351	16	US-10-410-913-30	Sequence 30, Appl
26	867	99.5	218	16	US-10-038-252-5	Sequence 5, Appli
27	865	99.3	1459	16	US-10-239-498A-4	Sequence 15, Appl
28	865	99.3	1459	16	US-10-239-498A-15	Sequence 9, Appli
29	846	97.1	160	15	US-10-298-796-9	GENERAL INFORMA
30	752	86.3	2319	14	US-10-187-319-6	Sequence 6, Appli
31	752	86.3	2319	14	US-10-131-510A-6	Sequence 4, Appli
32	736	84.5	1431	12	US-10-681-970-4	Sequence 4, Appli
33	736	84.5	1431	13	US-10-095-718-4	Sequence 39, Appl
34	720	82.7	1443	14	US-10-187-319-39	Sequence 39, Appl
35	720	82.7	1443	14	US-10-131-510A-39	Sequence 37, Appl
36	720	82.7	2133	14	US-10-187-319-37	Sequence 37, Appl
37	720	82.7	2133	14	US-10-131-510A-37	Sequence 1, Appli
38	683	78.4	130	15	US-10-298-796-1	Sequence 7, Appli
39	383	44.0	80	16	US-10-433-273-7	Sequence 4, Appli
40	380	43.6	218	16	US-10-038-252-4	Sequence 542, App
41	380	43.6	2224	16	US-10-741-601-542	Sequence 259, App
42	376	43.2	2196	15	US-10-360-101-259	Sequence 14, Appl
43	376	43.2	2224	14	US-10-115-563-14	Sequence 31, Appl
44	376	43.2	2224	14	US-10-172-712-31	Sequence 122, App
45	366.5	42.1	480	14	US-10-177-293-122	

ALIGNMENTS

RESULT 1
US-10-006-091-1
; Sequence 1, Application US/10006091
; Publication No. US20020102730A1
; GENERAL INFORMATION:
; APPLICANT: Cho, Myung-Sam
; APPLICANT: Chan, Sham-Yuen
; APPLICANT: Kelsey, William
; APPLICANT: Yee, Helena
; TITLE OF INVENTION: Expression System for Factor VIII
; FILE REFERENCE: MSB-7255.1
; CURRENT APPLICATION NUMBER: US/10/006,091
; CURRENT FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1438
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Derived from
; OTHER INFORMATION: human factor VIII sequence
US-10-006-091-1

Query Match	100.0%	Score 871;	DB 13;	Length 1438;
Best Local Similarity	100.0%;	Pred. No. 2.4e-90;		
Matches 164;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	CDLNSCSMPLGMSKAISDAQITASSYFTNNPATWSPSKARLHLOGRSNARWPQVNNPKE	60	
Db	1275	CDLNSCSMPLGMSKAISDAQITASSYFTNNPATWSPSKARLHLOGRSNARWPQVNNPKE	1334	
QY	61	WLQVDFQKMTKVTGVTQGVKSLTSMYVKEPLISSQDGHQHTLFFQNGKVKVFQGNQD	120	
Db	1335	WLQVDFQKMTKVTGVTQGVKSLTSMYVKEPLISSQDGHQHTLFFQNGKVKVFQGNQD	1394	
QY	121	SFTPVVNSLDPPLLTRYLEIHFQSWVHQIALRNEVLGCEAQDLY	164	

```
Db 1395 SFTPVNSLDPLLLTRYLRHQPQSWHQAIALRMEVLGCEAODLY 1438

RESULT 2
US-10-047-257-1
; Sequence 1, Application US/10047257
; Publication No. US20020115152A1
; GENERAL INFORMATION:
; APPLICANT: Cho, Myung-Sam
; APPLICANT: Chan, Sham-Yuen
; APPLICANT: Kelsey, William
; APPLICANT: Yee, Helena
; TITLE OF INVENTION: Expression System for Factor VIII
; FILE REFERENCE: MSB-7255.2
; CURRENT APPLICATION NUMBER: US/10/047,257
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1438
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Derived from
US-10-047-257-1

Query Match 100.0%; Score 871; DB 13; Length 1438;
Best Local Similarity 100.0%; Pred. No. 2.4e-90;
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 CDLNCSMPLGMESKAISSDAQITASSYFTNMFTWSPSKARLHLOGRSNARPOVNNPKE 60
Db 1275 CDLNCSMPLGMESKAISSDAQITASSYFTNMFTWSPSKARLHLOGRSNARPOVNNPKE 1334

Cy 61 WLQVDFQKTMKVTGTTQGVKSLLTSMYVKEFLISSQDGHQWTLFFQNGKVKVFGNQD 120
Db 1335 WLQVDFQKTMKVTGTTQGVKSLLTSMYVKEFLISSQDGHQWTLFFQNGKVKVFGNQD 1394

Cy 121 SFTPVNSLDPLLLTRYLRHQPQSWHQAIALRMEVLGCEAODLY 164
Db 1395 SFTPVNSLDPLLLTRYLRHQPQSWHQAIALRMEVLGCEAODLY 1438

RESULT 4
US-10-239-498A-13
; Sequence 13, Application US/10239498A
; Publication No. US2004002333A1
; GENERAL INFORMATION:
; APPLICANT: Hauser, Charlotte
; APPLICANT: Horster, Andrea
; APPLICANT: Schroder, Carola
; APPLICANT: Lehnerer, Michael
; TITLE OF INVENTION: Production of Recombinant Blood Clotting Factors in
; TITLE OF INVENTION: Human Cell Lines
; FILE REFERENCE: 80977.0001
; CURRENT APPLICATION NUMBER: US/10/239,498A
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: PCT/EP01/03220
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1459
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pTGF8-2hyg-s
US-10-239-498A-13

Query Match 100.0%; Score 871; DB 16; Length 1459;
Best Local Similarity 100.0%; Pred. No. 2.4e-90;
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 CDLNCSMPLGMESKAISSDAQITASSYFTNMFTWSPSKARLHLOGRSNARPOVNNPKE 60
Db 1296 CDLNCSMPLGMESKAISSDAQITASSYFTNMFTWSPSKARLHLOGRSNARPOVNNPKE 1355

Cy 61 WLQVDFQKTMKVTGTTQGVKSLLTSMYVKEFLISSQDGHQWTLFFQNGKVKVFGNQD 120
Db 1356 WLQVDFQKTMKVTGTTQGVKSLLTSMYVKEFLISSQDGHQWTLFFQNGKVKVFGNQD 1415

Cy 121 SFTPVNSLDPLLLTRYLRHQPQSWHQAIALRMEVLGCEAODLY 164
Db 1416 SFTPVNSLDPLLLTRYLRHQPQSWHQAIALRMEVLGCEAODLY 1459

RESULT 5
US-10-681-970-2
; Sequence 2, Application US/10681970
; Publication No. US20040062752A1
; GENERAL INFORMATION:
; APPLICANT: Walsh, Christopher
; APPLICANT: Chao, Hengjun
; APPLICANT: Burstein, Haim
; APPLICANT: Lynch, Carmel
; APPLICANT: Stepan, Tony
; APPLICANT: Munson, Keith
; TITLE OF INVENTION: Adeno-Associated Virus Vectors Encoding Factor VIII and
; FILE REFERENCE: Methods of Using the Same
; FILE REFERENCE: 35052/204375
; CURRENT APPLICATION NUMBER: US/10/681,970
; CURRENT FILING DATE: 2003-10-09
```

```
; PRIOR APPLICATION NUMBER: US/09/689,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/158,780
; PRIOR FILING DATE: 1999-10-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1471
; TYPE: PRT
; ORGANISM: Homo sapiens B-domain deleted factor VIII
; FEATURE:
; OTHER INFORMATION: Homo sapiens BDD FVIII
;
US-10-661-970-2

Query Match          100.0%; Score 871; DB 12; Length 1471;
Best Local Similarity 100.0%; Pred. No. 2.5e-90;
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CDLNSCMPLGWESKAISDAQITASSYFTNMFAWSPSKARLHQLGRSNARWPQVNNPKE 60
Db      1308 CDLNSCMPLGWESKAISDAQITASSYFTNMFAWSPSKARLHQLGRSNARWPQVNNPKE 1367

QY      61 WLQVDFQKTMKVGTGVTGQVKSLLTSMYKKEFLISSQDGHQWTLFFQNGKVKVFGNQD 120
Db      1368 WLQVDFQKTMKVGTGVTGQVKSLLTSMYKKEFLISSQDGHQWTLFFQNGKVKVFGNQD 1427

QY      121 SFTPVNSLDPPLLTRYLRHPQSWVHQIALRMEVLGCEAODLY 164
Db      1428 SFTPVNSLDPPLLTRYLRHPQSWVHQIALRMEVLGCEAODLY 1471

RESULT 6
US-10-095-718-2
; Sequence 2, Application US/10095718
; Publication No. US20020131956A1
; GENERAL INFORMATION:
; APPLICANT: Walsh, Christopher
; APPLICANT: Chao, Hengjun
; APPLICANT: Burstein, Haim
; APPLICANT: Lynch, Carmel
; APPLICANT: Stepan, Tony
; APPLICANT: Munson, Keith
; TITLE OF INVENTION: Adeno-Associated Virus Vectors Encoding Factor VIII and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 35052/204375
; CURRENT APPLICATION NUMBER: US/10/095,718
; CURRENT FILING DATE: 2002-03-12
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/158,780
; PRIOR FILING DATE: 1999-10-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1471
; TYPE: PRT
; ORGANISM: Homo sapiens B-domain deleted factor VIII
; FEATURE:
; OTHER INFORMATION: Homo sapiens BDD FVIII
;
US-10-095-718-2

Query Match          100.0%; Score 871; DB 13; Length 1471;
Best Local Similarity 100.0%; Pred. No. 2.5e-90;
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CDLNSCMPLGWESKAISDAQITASSYFTNMFAWSPSKARLHQLGRSNARWPQVNNPKE 60
Db      1308 CDLNSCMPLGWESKAISDAQITASSYFTNMFAWSPSKARLHQLGRSNARWPQVNNPKE 1367

QY      61 WLQVDFQKTMKVGTGVTGQVKSLLTSMYKKEFLISSQDGHQWTLFFQNGKVKVFGNQD 120
Db      1368 WLQVDFQKTMKVGTGVTGQVKSLLTSMYKKEFLISSQDGHQWTLFFQNGKVKVFGNQD 1427
```

```
QY      121 SFTPVNSLDPPLLTRYLRHPQSWVHQIALRMEVLGCEAODLY 164
Db      1428 SFTPVNSLDPPLLTRYLRHPQSWVHQIALRMEVLGCEAODLY 1471

RESULT 7
US-09-957-641-2
; Sequence 2, Application US/09957641
; Publication No. US20020182670A1
; GENERAL INFORMATION:
; APPLICANT: Emory University
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: 75-00
; CURRENT APPLICATION NUMBER: US/09/957,641
; CURRENT FILING DATE: 2001-09-16
; PRIOR APPLICATION NUMBER: US 60/234047
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: US 60/236460
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2332
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-09-957-641-2

Query Match          100.0%; Score 871; DB 9; Length 2332;
Best Local Similarity 100.0%; Pred. No. 4.6e-90;
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CDLNSCMPLGWESKAISDAQITASSYFTNMFAWSPSKARLHQLGRSNARWPQVNNPKE 60
Db      2169 CDLNSCMPLGWESKAISDAQITASSYFTNMFAWSPSKARLHQLGRSNARWPQVNNPKE 2228

QY      61 WLQVDFQKTMKVGTGVTGQVKSLLTSMYKKEFLISSQDGHQWTLFFQNGKVKVFGNQD 120
Db      2229 WLQVDFQKTMKVGTGVTGQVKSLLTSMYKKEFLISSQDGHQWTLFFQNGKVKVFGNQD 2288

QY      121 SFTPVNSLDPPLLTRYLRHPQSWVHQIALRMEVLGCEAODLY 164
Db      2289 SFTPVNSLDPPLLTRYLRHPQSWVHQIALRMEVLGCEAODLY 2332

RESULT 8
US-10-187-319-2
; Sequence 2, Application US/10187319
; Publication No. US20030068785A1
; GENERAL INFORMATION:
; APPLICANT: Lollar, John S.
; TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle Suite 201
; CITY: Boulder
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80303
;
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/187,319
FILING DATE: 27-Aug-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/523,656
FILING DATE: 2000-03-10
APPLICATION NUMBER: US 09/037,601
FILING DATE: 1998-03-10
```

```

; APPLICATION NUMBER: WO PCT/US97/11155
; FILING DATE: 1997-06-26
; APPLICATION NUMBER: US 08/670,707
; FILING DATE: 1996-06-26
; ATTORNEY/AGENT INFORMATION:
; NAME: Greenlee, Lorance L.
; REGISTRATION NUMBER: 27,894
; REFERENCE/DOCKET NUMBER: 75-95K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303/499-8080
; TELEFAX: 303/499-8089
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2332 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: <Unknown>
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: Liver
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-187-319-2

Query Match 100.0%; Score 871; DB 14; Length 2332;
Best Local Similarity 100.0%; Pred. No. 4.6e-90;
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDLNSCSMPGLGMSKATSDAQITASSYFTNMFWATWSPSKARLHLOGRSNARPOVNNPKE 60
Db 2169 CDLNSCSMPGLGMSKATSDAQITASSYFTNMFWATWSPSKARLHLOGRSNARPOVNNPKE 2228

Qy 61 WLQVDFQKTMKVGTGTQGVKSLLTSMYVKEFLISSQDGHQWTLFFQNGKVKVFGNQD 120
Db 2229 WLQVDFQKTMKVGTGTQGVKSLLTSMYVKEFLISSQDGHQWTLFFQNGKVKVFGNQD 2288

Qy 121 SFTPVNSLDPPLLTRYLRHPQSWVHQIALRMEVLGCEAODLY 164
Db 2289 SFTPVNSLDPPLLTRYLRHPQSWVHQIALRMEVLGCEAODLY 2332

RESULT 9
US-10-131-510A-2
; Sequence 2, Application US/10131510A
; Publication No. US20030166536A1
; GENERAL INFORMATION:
; APPLICANT: Lollar, John S
; TITLE OF INVENTION: Modified Factor VIII
; FILE REFERENCE: 75-95J
; CURRENT APPLICATION NUMBER: US/10/131,510A
; PRIOR FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: U.S. 09/315,179
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: U.S. 09/037,601
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: U.S. 08/670,707
; PRIOR FILING DATE: 1996-06-26
; PRIOR APPLICATION NUMBER: PCT/US97/11155
; PRIOR FILING DATE: 1997-06-26
; PRIOR APPLICATION NUMBER: PCT/US94/13200
; PRIOR FILING DATE: 1994-11-15
; PRIOR APPLICATION NUMBER: U.S. 08/212,133
; PRIOR FILING DATE: 1994-03-11
; PRIOR APPLICATION NUMBER: U.S. 07/864,004
; PRIOR FILING DATE: 1992-04-07
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2332
; TYPE: PRT

```

```

; ORGANISM: Homo sapiens
; US-10-131-510A-2

Query Match 100.0%; Score 871; DB 14; Length 2332;
Best Local Similarity 100.0%; Pred. No. 4.6e-90;
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDLNSCSMPGLGMSKATSDAQITASSYFTNMFWATWSPSKARLHLOGRSNARPOVNNPKE 60
Db 2169 CDLNSCSMPGLGMSKATSDAQITASSYFTNMFWATWSPSKARLHLOGRSNARPOVNNPKE 2228

Qy 61 WLQVDFQKTMKVGTGTQGVKSLLTSMYVKEFLISSQDGHQWTLFFQNGKVKVFGNQD 120
Db 2229 WLQVDFQKTMKVGTGTQGVKSLLTSMYVKEFLISSQDGHQWTLFFQNGKVKVFGNQD 2288

Qy 121 SFTPVNSLDPPLLTRYLRHPQSWVHQIALRMEVLGCEAODLY 164
Db 2289 SFTPVNSLDPPLLTRYLRHPQSWVHQIALRMEVLGCEAODLY 2332

RESULT 10
US-10-445-235-2
; Sequence 2, Application US/10445235
; Publication No. US20040005670A1
; GENERAL INFORMATION:
; APPLICANT: Katherine A. High
; APPLICANT: Rodney M. Camire
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: TREATMENT OF HEMOPHILIA A
; FILE REFERENCE: CHOP0176
; CURRENT APPLICATION NUMBER: US/10/445,235
; CURRENT FILING DATE: 2003-05-22
; PRIOR APPLICATION NUMBER: 60/382,486
; PRIOR FILING DATE: 2002-05-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 2332
; TYPE: PRT
; ORGANISM: homo sapiens
; US-10-445-235-2

Query Match 100.0%; Score 871; DB 15; Length 2332;
Best Local Similarity 100.0%; Pred. No. 4.6e-90;
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDLNSCSMPGLGMSKATSDAQITASSYFTNMFWATWSPSKARLHLOGRSNARPOVNNPKE 60
Db 2169 CDLNSCSMPGLGMSKATSDAQITASSYFTNMFWATWSPSKARLHLOGRSNARPOVNNPKE 2228

Qy 61 WLQVDFQKTMKVGTGTQGVKSLLTSMYVKEFLISSQDGHQWTLFFQNGKVKVFGNQD 120
Db 2229 WLQVDFQKTMKVGTGTQGVKSLLTSMYVKEFLISSQDGHQWTLFFQNGKVKVFGNQD 2288

Qy 121 SFTPVNSLDPPLLTRYLRHPQSWVHQIALRMEVLGCEAODLY 164
Db 2289 SFTPVNSLDPPLLTRYLRHPQSWVHQIALRMEVLGCEAODLY 2332

RESULT 11
US-10-360-101-229
; Sequence 229, Application US/10360101
; Publication No. US20040009550A1
; GENERAL INFORMATION:
; APPLICANT: Moll, Gert N.
; APPLICANT: Leenhouts, Cornelis J.
; TITLE OF INVENTION: Export and modification of (poly)peptide in the lantibiotic way
; FILE REFERENCE: 2183-5673
; CURRENT APPLICATION NUMBER: US/10/360,101
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: EP 02077060.8
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 309

```



```
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 229
; LENGTH: 2332
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sequence of factor VIII
US-10-360-101-229

Query Match      100.0%; Score 871; DB 15; Length 2332;
Best Local Similarity 100.0%; Pred. No. 4.6e-90;
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDLNSCSMPGLGMSKAISSDAQITASSYFTNMFTATWSKARLHLQGRSNARPPQVNNPKE 60
DB 2169 CDLNSCSMPGLGMSKAISSDAQITASSYFTNMFTATWSKARLHLQGRSNARPPQVNNPKE 2228

QY 61 WLQVDFQKTMKVGTGTTQGVKSLLTSMYVKEFLISSQDGHQWTLFFQNGKVKVFGNQD 120
DB 2229 WLQVDFQKTMKVGTGTTQGVKSLLTSMYVKEFLISSQDGHQWTLFFQNGKVKVFGNQD 2288

QY 121 SFTPVNSLDPPLLTRYLRIHPQSWHQAIALRMEVLGCEAQLDLY 164
DB 2289 SFTPVNSLDPPLLTRYLRIHPQSWHQAIALRMEVLGCEAQLDLY 2332

RESULT 12
US-10-239-498A-2
; Sequence 2, Application US/10239498A
; Publication No. US2004002333A1
; GENERAL INFORMATION:
; APPLICANT: Hauser, Charlotte
; APPLICANT: Horster, Andrea
; APPLICANT: Schroder, Carola
; APPLICANT: Lehnerer, Michael
; TITLE OF INVENTION: Production of Recombinant Blood Clotting Factors in
; TITLE OF INVENTION: Human Cell Lines
; FILE REFERENCE: 80977.0001
; CURRENT APPLICATION NUMBER: US/10/239,498A
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: PCT/EP01/03220
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2332
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-239-498A-2

Query Match      100.0%; Score 871; DB 16; Length 2332;
Best Local Similarity 100.0%; Pred. No. 4.6e-90;
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDLNSCSMPGLGMSKAISSDAQITASSYFTNMFTATWSKARLHLQGRSNARPPQVNNPKE 60
DB 2169 CDLNSCSMPGLGMSKAISSDAQITASSYFTNMFTATWSKARLHLQGRSNARPPQVNNPKE 2228

QY 61 WLQVDFQKTMKVGTGTTQGVKSLLTSMYVKEFLISSQDGHQWTLFFQNGKVKVFGNQD 120
DB 2229 WLQVDFQKTMKVGTGTTQGVKSLLTSMYVKEFLISSQDGHQWTLFFQNGKVKVFGNQD 2288

QY 121 SFTPVNSLDPPLLTRYLRIHPQSWHQAIALRMEVLGCEAQLDLY 164
DB 2289 SFTPVNSLDPPLLTRYLRIHPQSWHQAIALRMEVLGCEAQLDLY 2332

RESULT 13
US-10-466-998A-1
; Sequence 1, Application US/10466998A
; Publication No. US20040126856A1
; GENERAL INFORMATION:
; APPLICANT: BAJAJ, S. Paul
```

```
; APPLICANT: FAY, Philip J.
; TITLE OF INVENTION: Factor IXa: Factor VIIa Interaction and Methods
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: 66153-41436
; CURRENT APPLICATION NUMBER: US/10/466,998A
; CURRENT FILING DATE: 2004-01-15
; PRIOR APPLICATION NUMBER: PCT/US02/01724
; PRIOR FILING DATE: 2002-01-23
; PRIOR APPLICATION NUMBER: US 60/263,431
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2332
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-466-998A-1

Query Match      100.0%; Score 871; DB 16; Length 2332;
Best Local Similarity 100.0%; Pred. No. 4.6e-90;
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDLNSCSMPGLGMSKAISSDAQITASSYFTNMFTATWSKARLHLQGRSNARPPQVNNPKE 60
DB 2169 CDLNSCSMPGLGMSKAISSDAQITASSYFTNMFTATWSKARLHLQGRSNARPPQVNNPKE 2228

QY 61 WLQVDFQKTMKVGTGTTQGVKSLLTSMYVKEFLISSQDGHQWTLFFQNGKVKVFGNQD 120
DB 2229 WLQVDFQKTMKVGTGTTQGVKSLLTSMYVKEFLISSQDGHQWTLFFQNGKVKVFGNQD 2288

QY 121 SFTPVNSLDPPLLTRYLRIHPQSWHQAIALRMEVLGCEAQLDLY 164
DB 2289 SFTPVNSLDPPLLTRYLRIHPQSWHQAIALRMEVLGCEAQLDLY 2332

RESULT 14
US-10-411-037-30
; Sequence 30, Application US/10411037
; Publication No. US20040043446A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryn
; TITLE OF INVENTION: ALPHA GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA
; TITLE OF INVENTION: GALACTOSIDASE A
; FILE REFERENCE: 040853-01-5082
; CURRENT APPLICATION NUMBER: US/10/411,037
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 30
; LENGTH: 2351
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-411-037-30
```

Search completed: September 29, 2004, 16:51:38
Job time : 132 secs

Query Match 100.0%; Score 871; DB 12; Length 2351;
Best Local Similarity 100.0%; Pred. No. 4.7e-90;
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDLNSCSMPGLGMSKASDAQITASSYFTNMFATWSPSKARLHLOGRSNARFPQVNNPKE 60
DB 2188 CDLNSCSMPGLGMSKASDAQITASSYFTNMFATWSPSKARLHLOGRSNARFPQVNNPKE 2247
QY 61 WLQVDFQKTMKVTGVTTCQGVKSLTSMYVKEFLISSQDGHQWTLFFQNGKVKVFGNQD 120
DB 2248 WLQVDFQKTMKVTGVTTCQGVKSLTSMYVKEFLISSQDGHQWTLFFQNGKVKVFGNQD 2307
QY 121 SFTPVNSLDPLLTRYLRIHQSWVHQIALRMEVLGCEAQLDY 164
DB 2308 SFTPVNSLDPLLTRYLRIHQSWVHQIALRMEVLGCEAQLDY 2351

RESULT 15

US-10-411-026-30
; Sequence 30, Application US/10411026
; Publication No. US20040063911A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zepf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; TITLE OF INVENTION: PROTEIN REMODELING METHODS AND PEPTIDES PRODUCED BY THE
; FILE REFERENCE: 040853-01-5053
; CURRENT APPLICATION NUMBER: US/10/411,026
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 30
; LENGTH: 2351
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-411-026-30

Query Match 100.0%; Score 871; DB 12; Length 2351;
Best Local Similarity 100.0%; Pred. No. 4.7e-90;
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDLNSCSMPGLGMSKASDAQITASSYFTNMFATWSPSKARLHLOGRSNARFPQVNNPKE 60
DB 2188 CDLNSCSMPGLGMSKASDAQITASSYFTNMFATWSPSKARLHLOGRSNARFPQVNNPKE 2247
QY 61 WLQVDFQKTMKVTGVTTCQGVKSLTSMYVKEFLISSQDGHQWTLFFQNGKVKVFGNQD 120
DB 2248 WLQVDFQKTMKVTGVTTCQGVKSLTSMYVKEFLISSQDGHQWTLFFQNGKVKVFGNQD 2307
QY 121 SFTPVNSLDPLLTRYLRIHQSWVHQIALRMEVLGCEAQLDY 164
DB 2308 SFTPVNSLDPLLTRYLRIHQSWVHQIALRMEVLGCEAQLDY 2351

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 29, 2004, 16:35:13 ; Search time 13 seconds
(without alignments)
656.895 Million cell updates/sec

Title: US-10-049-399A-1_COPY_2169_2332

Perfect score: 871

Sequence: 1 CDLNSCMPLGHSKASDA.....VHQIALRMVLCGCAQDLY 164

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	871	100.0	2351	1	FA8_HUMAN
2	752	86.3	2319	1	FA8_MOUSE
3	720	82.7	2133	1	FA8_PIG
4	385	44.2	2258	1	FA5_PIG
5	379	43.5	2211	1	FA5_BOVIN
6	376	43.2	2224	1	FA5_HUMAN
7	367.5	42.2	427	1	MFGM_MOUSE
8	353.5	40.6	463	1	MFGM_MOUSE
9	329	37.8	925	1	NRP2_MOUSE
10	328.5	37.7	409	1	MFGM_PIG
11	327.5	37.6	387	1	MFGM_HUMAN
12	327	37.5	931	1	NRP2_HUMAN
13	327	37.5	931	1	NRP2_MOUSE
14	324.5	37.3	427	1	MFGM_BOVIN
15	275.5	31.6	914	1	NRP1_CHICK
16	269.5	30.9	923	1	NRP1_MOUSE
17	266	30.5	764	1	CPX2_MOUSE
18	265.5	30.5	922	1	NRP1_MOUSE
19	265.5	30.5	923	1	NRP1_HUMAN
20	261	30.0	756	1	CPX2_HUMAN
21	256	29.4	280	1	XLRI_FUGRU
22	254.5	29.2	928	1	NRP1_XENLA
23	247	28.4	224	1	XLRI_MOUSE
24	243	27.9	224	1	XLRI_HUMAN
25	234.5	26.9	3133	1	HMCT_BOMMO
26	217	24.9	1331	1	CTA2_HUMAN
27	215.5	24.7	722	1	CPXM_MOUSE
28	214	24.6	734	1	CPXM_HUMAN
29	208	23.9	1310	1	CTA4_MOUSE
30	206	23.7	1308	1	CTA4_HUMAN
31	199	22.8	909	1	DDR1_PANTR
32	194	22.3	1288	1	CTA3_HUMAN
33	192	22.0	913	1	DDR1_HUMAN

34	184	21.1	1284	1	NRX4_DROME
35	183	21.0	910	1	DDR1_RAT
36	183	21.0	911	1	DDR1_MOUSE
37	181	20.8	1384	1	CTA1_HUMAN
38	180.5	20.7	854	1	DDR2_MOUSE
39	176.5	20.3	855	1	DDR2_HUMAN
40	171	19.6	1381	1	CTA1_RAT
41	171	19.6	1385	1	CTA1_MOUSE
42	107.5	12.3	257	1	DIS2_DICDI
43	104	11.9	867	1	SSPO_BOVIN
44	84.5	9.7	149	1	DISP_DICDI
45	84.5	9.7	253	1	DISC_DICDI

ALIGNMENTS

RESULT 1	
FA8_HUMAN	
ID	FA8_HUMAN
AC	P00451;
DT	21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DT	10-OCT-2003 (Rel. 42, Last annotation update)
DE	Coagulation factor VIII precursor (Procoagulant component)
DE	(Antihemophilic factor) (AHF).
GN	F8 OR F8C.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
OR	[1]
RP	SEQUENCE FROM N.A.
RP	MEDLINE=86081164; PubMed=3935400;
RA	Truett M.A., Blacher R., Burke R.L., Caput D., Chu C., Dina D.,
RA	Hartog K., Kuo C.H., Maslary F.R., Merryweather J.P., Najarian R.,
RA	Pachl C., Potter S.J., Puma J., Quiroga M., Rall L.B., Randolph A.,
RA	Urdea M.S., Valenzuela P., Dahl H.H.M., Favalaro J., Hansen J.,
RA	Nordfang O., Ezban M.
RT	"Characterization of the polypeptide composition of human factor
RT	VIII:C and the nucleotide sequence and expression of the human kidney
RT	cDNA."
RL	DNA 4:333-349(1985).
RN	[2]
RP	SEQUENCE FROM N.A.
RP	MEDLINE=85061548; PubMed=6438526;
RA	Wood W.I., Capon D.J., Simonsen C.C., Eaton D.L., Gitschier J.,
RA	Key B., Seeburg P.H., Smith D.H., Hollingshead P., Wion K.L.,
RA	Delwart E., Tuddenham E.G.D., Vehar G.A., Lawn R.M.
RT	"Expression of active human factor VIII from recombinant DNA clones."
RL	Nature 312:330-337(1984).
RN	[3]
RP	SEQUENCE FROM N.A.
RP	MEDLINE=85061550; PubMed=6438528;
RA	Toole J.J., Knopf J.L., Wozney J.M., Sultzman L.A., Buecker J.L.,
RA	Pittman D.D., Kaufman R.J., Brown E., Shoemaker C., Orr E.C.,
RA	Amphlett G.W., Foster W.B., Coe M.L., Knutson G.J., Pass D.N.,
RA	Hewick R.M.
RT	"Molecular cloning of a cDNA encoding human antihemophilic factor."
RL	Nature 312:342-347(1984).
RN	[4]
RP	SEQUENCE FROM N.A.
RP	MEDLINE=93265012; PubMed=1303178;
RA	Gitschier J., Wood W.I.
RT	"Sequence of the exon-containing regions of the human factor VIII
RT	gene."
RL	Hum. Mol. Genet. 1:199-200(1992).
RN	[5]
RP	SEQUENCE OF 2064-2070 FROM N.A.
RA	de Water N.S., Williams R., Browett P.J.
RA	Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN	[6]
RP	SULFATION OF TYR-1699.

RX MEDLINE=91093266; PubMed=1898735;
 RA Leyte A., van Schijndel H.B., Niehrs C., Huttner W.B., Verbeet M.P.,
 RA Mertens K., van Mourik J.A.;
 RT "Sulfation of Tyr1680 of human blood coagulation factor VIII is
 RT essential for the interaction of factor VIII with von Willebrand
 RT factor.";
 RL J. Biol. Chem. 266:740-746(1991).
 RN [7]
 RP VARIANT HEMA GYS-391.
 RX MEDLINE=92207952; PubMed=1554716;
 RA Pitman D.D., Wang J.H., Kaufman R.J.;
 RT "Identification and functional importance of tyrosine sulfate
 RT residues within recombinant factor VIII.";
 RN Biochemistry 31:3315-3325(1992).
 RN [8]
 RP STRUCTURE BY NMR OF 2322-2343.
 RX MEDLINE=95200924; PubMed=7893714;
 RA Gilbert G.E., Baleja J.D.;
 RT "Membrane-binding peptide from the C2 domain of factor VIII forms an
 RT amphipathic structure as determined by NMR spectroscopy.";
 RN Biochemistry 34:3022-3031(1995).
 RN [9]
 RP REVIEW ON MOLECULAR BASIS OF HEMA.
 RX MEDLINE=91221499; PubMed=1902642;
 RA Gitschier J.;
 RT "The molecular basis of hemophilia A.";
 RL Ann. N.Y. Acad. Sci. 614:89-96(1991).
 RN [10]
 RP REVIEW ON MOLECULAR BASIS OF HEMA.
 RX MEDLINE=89088506; PubMed=2491949;
 RA White G.C. II, Shoemaker C.B.;
 RT "Factor VIII gene and hemophilia A.";
 RL Blood 73:1-12(1989).
 RN [11]
 RP REVIEW ON MOLECULAR BASIS OF HEMA.
 RX MEDLINE=95245332; PubMed=7728145;
 RA Antonarakis S.E., Kazazian H.H., Tuddenham E.G.D.;
 RT "Molecular etiology of factor VIII deficiency in hemophilia A.";
 RL Hum. Mutat. 5:1-22(1995).
 RN [12]
 RP VARIANT HEMA GLN-2326.
 RX MEDLINE=86235434; PubMed=3012775;
 RA Gitschier J., Wood W.I., Shuman M.A., Lawn R.M.;
 RT "Identification of a missense mutation in the factor VIII gene of a
 RT mild hemophiliac.";
 RL Science 232:1415-1416(1986).
 RN [13]
 RP VARIANT HEMA PRO-2135.
 RX MEDLINE=88096539; PubMed=3122181;
 RA Levinson B., Janco R.L., Phillips J.A. III, Gitschier J.;
 RT "A novel missense mutation in the factor VIII gene identified by
 RT analysis of amplified hemophilia DNA sequences.";
 RL Nucleic Acids Res. 15:9797-9805(1987).
 RN [14]
 RP VARIANT HEMA GLN-2228.
 RX MEDLINE=88191889; PubMed=2833855;
 RA Youssoufian H., Antonarakis S.E., Bell W., Griffin A.M.,
 RA Kazazian H.H.;
 RT "Nonsense and missense mutations in hemophilia A: estimate of the
 RT relative mutation rate at CG dinucleotides.";
 RL Am. J. Hum. Genet. 42:718-725(1988).
 RN [15]
 RP VARIANT HEMA GYS-291.
 RX MEDLINE=88220354; PubMed=2835904;
 RA Youssoufian H., Wong C., Aronis S., Platakoukis H., Kazazian H.H. Jr.,
 RA Antonarakis S.E.;
 RT "Moderately severe hemophilia A resulting from Glu-->Gly substitution
 RT in exon 7 of the factor VIII gene.";
 RL Am. J. Hum. Genet. 42:867-871(1988).
 RN [16]
 RP VARIANT HEMA GYS-1708.
 RX MEDLINE=89274393; PubMed=2499363;
 RA O'Brien D.P., Tuddenham E.G.;
 RT "Purification and characterization of factor VIII 1,689-Cys: a
 RT nonfunctional cofactor occurring in a patient with severe hemophilia
 RT A.";
 RL Blood 73:2117-2122(1989).
 RN [17]
 RP VARIANT HEMA GYS-391.
 RX MEDLINE=90001543; PubMed=2506948;
 RA Shima M., Ware J., Yoshioka A., Fukui H., Fulcher C.A.;
 RT "An arginine to cysteine amino acid substitution at a critical
 RT thrombin cleavage site in a dysfunctional factor VIII molecule.";
 RL Blood 74:1612-1617(1989).
 RN [18]
 RP VARIANT HEMA LEU-189.
 RX MEDLINE=90057680; PubMed=2510835;
 RA Chan V., Chan T.K., Tong T.M., Todd D.;
 RT "A novel missense mutation in exon 4 of the factor VIII:C gene
 RT resulting in moderately severe hemophilia A.";
 RL Blood 74:2688-2691(1989).
 RN [19]
 RP VARIANT HEMA LEU-2326.
 RX MEDLINE=89197216; PubMed=2495245;
 RA Inaba H., Fujimaki M., Kazazian H.H. Jr., Antonarakis S.E.;
 RT "Mild hemophilia A resulting from Arg-to-Leu substitution in exon 26
 RT of the factor VIII gene.";
 RL Hum. Genet. 81:335-338(1989).
 RN [20]
 RP VARIANT HEMA HIS-391.
 RX MEDLINE=89264602; PubMed=2498882;
 RA Arai M., Inaba H., Higuchi M., Antonarakis S.E., Kazazian H.H. Jr.,
 RA Fujimaki M., Hoyer L.W.;
 RT "Direct characterization of factor VIII in plasma: detection of a
 RT mutation altering a thrombin cleavage site
 RT (arginine-372-->histidine).";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:4277-4281(1989).
 RN [21]
 RP VARIANT HEMA GYS-1708.
 RX MEDLINE=90105723; PubMed=2104766;
 RA Arai M., Higuchi M., Antonarakis S.E., Kazazian H.H. Jr.,
 RA Phillips J.A. III, Janco R.L., Hoyer L.W.;
 RT "Characterization of a thrombin cleavage site mutation (Arg 1689 to
 RT Cys) in the factor VIII gene of two unrelated patients with
 RT cross-reacting material-positive hemophilia A.";
 RL Blood 75:384-389(1990).
 RN [22]
 RP VARIANTS HEMA GLN-2228 AND LEU-2326.
 RX MEDLINE=90123183; PubMed=2105106;
 RA Casula L., Murru S., Pecorara M., Ristaldi M.S., Restagno G.,
 RA Mancuso G., Morfini M., de Biasi R., Baudo F., Carbonara A.;
 RT "Recurrent mutations and three novel rearrangements in the factor
 RT VIII gene of hemophilia A patients of Italian descent.";
 RL Blood 75:662-670(1990).
 RN [23]
 RP VARIANT HEMA GYS-391.
 RX MEDLINE=90329422; PubMed=1973901;
 RA Pattinson J.K., McVey J.H., Boon M., Ajani A., Tuddenham E.G.;
 RT "CRM+ hemophilia A due to a missense mutation (372-->Cys) at the
 RT internal heavy chain thrombin cleavage site.";
 RL Br. J. Haematol. 75:73-77(1990).
 RN [24]
 RP VARIANTS HEMA PHE-1699 AND GYS-1708.
 RX MEDLINE=90152691; PubMed=2105906;
 RA Higuchi M., Wong C., Kochhan L., Olek K., Aronis S., Kasper C.K.,
 RA Kazazian H.H., Antonarakis S.E.;
 RT "Characterization of mutations in the factor VIII gene by direct
 RT sequencing of amplified genomic DNA.";
 RL Genomics 6:65-71(1990).
 RN [25]
 RP VARIANTS HEMA GYS-1728 AND ASP-1941.
 RX MEDLINE=90169988; PubMed=2106480;
 RA Traystman M.D., Higuchi M., Kasper C.K., Antonarakis S.E.,
 RA Kazazian H.H.;
 RT "Use of denaturing gradient gel electrophoresis to detect point
 RT mutations in the factor VIII gene."

	CHAIN	20	2319	COAGULATION FACTOR VIII.					
FT	DOMAIN	20	349	F5/8 TYPE A 1.					
FT	DOMAIN	20	199	PLASTOCYANIN-LIKE 1.					
FT	DOMAIN	207	349	PLASTOCYANIN-LIKE 2.					
FT	DOMAIN	399	730	F5/8 TYPE A 2.					
FT	DOMAIN	399	573	PLASTOCYANIN-LIKE 3.					
FT	DOMAIN	583	730	PLASTOCYANIN-LIKE 4.					
FT	DOMAIN	760	1640	B					
FT	DOMAIN	1683	2008	F5/8 TYPE A 3.				(BY SIMILARITY).	
FT	DOMAIN	1683	1845	PLASTOCYANIN-LIKE 5.				(BY SIMILARITY).	
FT	DOMAIN	1855	2008	PLASTOCYANIN-LIKE 6.				(BY SIMILARITY).	
FT	DOMAIN	2008	2156	F5/8 TYPE C 1.				(BY SIMILARITY).	
FT	DOMAIN	2161	2313	F5/8 TYPE C 2.				(BY SIMILARITY).	
FT	SITE	391	392	CLEAVAGE (BY THROMBIN)				(BY SIMILARITY).	
FT	SITE	759	760	CLEAVE (BY THROMBIN)				(BY SIMILARITY).	
FT	SITE	1678	1679	CLEAVE (BY THROMBIN)				(BY SIMILARITY).	
FT	SITE	1324	1325	CLEAVE (ACTIVATION)				(BY SIMILARITY).	
FT	SITE	1640	1641	CLEAVE (ACTIVATION)				(BY SIMILARITY).	
FT	MOD_RES	367	367	SULFATION (BY SIMILARITY).				(BY SIMILARITY).	
FT	MOD_RES	737	737	SULFATION (BY SIMILARITY).				(BY SIMILARITY).	
FT	MOD_RES	738	738	SULFATION (BY SIMILARITY).				(BY SIMILARITY).	
FT	MOD_RES	742	742	SULFATION (BY SIMILARITY).				(BY SIMILARITY).	
FT	MOD_RES	1669	1669	SULFATION (REQUIRED FOR VMF BINDING)				(BY SIMILARITY).	
FT	MOD_RES	1687	1687	SULFATION (BY SIMILARITY).				(BY SIMILARITY).	
FT	DISULFID	173	199	PROBABLE.				(POTENTIAL).	
FT	DISULFID	547	573	PROBABLE.				(POTENTIAL).	
FT	DISULFID	1819	1845	PROBABLE.				(POTENTIAL).	
FT	DISULFID	2008	2156	BY SIMILARITY.				(POTENTIAL).	
FT	DISULFID	2161	2313	BY SIMILARITY.				(POTENTIAL).	
FT	CARBOHYD	61	61	N-LINKED (GLCNAC.)				(POTENTIAL).	
FT	CARBOHYD	233	233	N-LINKED (GLCNAC.)				(POTENTIAL).	
FT	CARBOHYD	259	259	N-LINKED (GLCNAC.)				(POTENTIAL).	
FT	CARBOHYD	423	423	N-LINKED (GLCNAC.)				(POTENTIAL).	
FT	CARBOHYD	601	601	N-LINKED (GLCNAC.)				(POTENTIAL).	
FT	CARBOHYD	880	880	N-LINKED (GLCNAC.)				(POTENTIAL).	
FT	CARBOHYD	958	958	N-LINKED (GLCNAC.)				(POTENTIAL).	
FT	CARBOHYD	1015	1015	N-LINKED (GLCNAC.)				(POTENTIAL).	
FT	CARBOHYD	1022	1022	N-LINKED (GLCNAC.)				(POTENTIAL).	
FT	CARBOHYD	1026	1026	N-LINKED (GLCNAC.)				(POTENTIAL).	
FT	CARBOHYD	1044	1044	N-LINKED (GLCNAC.)				(POTENTIAL).	
FT	CARBOHYD	1076	1076	N-LINKED (GLCNAC.)				(POTENTIAL).	
FT	CARBOHYD	1087	1087	N-LINKED (GLCNAC.)				(POTENTIAL).	
FT	CARBOHYD	1136	1136	N-LINKED (GLCNAC.)				(POTENTIAL).	
FT	CARBOHYD	1161	1161	N-LINKED (GLCNAC.)				(POTENTIAL).	
FT	CARBOHYD	1192	1192	N-LINKED (GLCNAC.)				(POTENTIAL).	
FT	CARBOHYD	1255	1255	N-LINKED (GLCNAC.)				(POTENTIAL).	
FT	CARBOHYD	1268	1268	N-LINKED (GLCNAC.)				(POTENTIAL).	
FT	CARBOHYD	1273	1273	N-LINKED (GLCNAC.)				(POTENTIAL).	
FT	CARBOHYD	1274	1274	N-LINKED (GLCNAC.)				(POTENTIAL).	
FT	CARBOHYD	1302	1302	N-LINKED (GLCNAC.)				(POTENTIAL).	
FT	CARBOHYD	1316	1316	N-LINKED (GLCNAC.)				(POTENTIAL).	
FT	CARBOHYD	1340	1340	N-LINKED (GLCNAC.)				(POTENTIAL).	
FT	CARBOHYD	1378	1378	N-LINKED (GLCNAC.)				(POTENTIAL).	
FT	CARBOHYD	1797	1797	N-LINKED (GLCNAC.)				(POTENTIAL).	
FT	CARBOHYD	2105	2105	N-LINKED (GLCNAC.)				(POTENTIAL).	
FT	SEQUENCE	2319 AA;	2566148 MW;	FD054DBE051DB2A01 CRC64;					
Query Match		86.3%;	Score 752;	DB 1; Length 2319;					
Best Local Similarity		84.1%;	Pred. No. 1.3e-64;						
Matches 138;	Conservative	11;	Mismatches 15;	Indels 0; Gaps 0;					
Qy	1	CDLNSCSPLGMSKAISSDAQTASSYFTNNFATSPSKAPLHLQGRSNAWRPVNNPKPE	60						

FT	CHAIN	20	2319	COAGULATION FACTOR VIII.	
FT	DOMAIN	20	349	F5/8 TYPE A 1.	(BY SIMILARITY).
FT	DOMAIN	20	199	PLASTOCYANIN-LIKE 1.	(BY SIMILARITY).
FT	DOMAIN	207	349	PLASTOCYANIN-LIKE 2.	(BY SIMILARITY).
FT	DOMAIN	399	730	F5/8 TYPE A 2.	(BY SIMILARITY).
FT	DOMAIN	399	573	PLASTOCYANIN-LIKE 3.	(BY SIMILARITY).
FT	DOMAIN	583	730	PLASTOCYANIN-LIKE 4.	(BY SIMILARITY).
FT	DOMAIN	760	1640	B	(BY SIMILARITY).
FT	DOMAIN	1683	2008	F5/8 TYPE A 3.	(BY SIMILARITY).
FT	DOMAIN	1683	1845	PLASTOCYANIN-LIKE 5.	(BY SIMILARITY).
FT	DOMAIN	1855	2008	PLASTOCYANIN-LIKE 6.	(BY SIMILARITY).
FT	DOMAIN	2008	2156	F5/8 TYPE C 1.	(BY SIMILARITY).
FT	DOMAIN	2161	2313	F5/8 TYPE C 2.	(BY SIMILARITY).
FT	SITE	391	392	CLEAVAGE (BY THROMBIN)	(BY SIMILARITY).
FT	SITE	759	760	CLEAVE (BY THROMBIN)	(BY SIMILARITY).
FT	SITE	1678	1679	CLEAVE (BY THROMBIN)	(BY SIMILARITY).
FT	SITE	1324	1325	CLEAVE (ACTIVATION)	(BY SIMILARITY).
FT	SITE	1640	1641	CLEAVE (ACTIVATION)	(BY SIMILARITY).
FT	MOD_RES	367	367	SULFATION (BY SIMILARITY).	(BY SIMILARITY).
FT	MOD_RES	737	737	SULFATION (BY SIMILARITY).	(BY SIMILARITY).
FT	MOD_RES	738	738	SULFATION (BY SIMILARITY).	(BY SIMILARITY).
FT	MOD_RES	742	742	SULFATION (BY SIMILARITY).	(BY SIMILARITY).
FT	MOD_RES	1669	1669	SULFATION (REQUIRED FOR VMF BINDING)	(BY SIMILARITY).
FT	MOD_RES	1687	1687	SULFATION (BY SIMILARITY).	(BY SIMILARITY).
FT	DISULFID	173	199	PROBABLE.	(BY SIMILARITY).
FT	DISULFID	547	573	PROBABLE.	(BY SIMILARITY).
FT	DISULFID	1819	1845	PROBABLE.	(BY SIMILARITY).
FT	DISULFID	2008	2156	BY SIMILARITY.	(BY SIMILARITY).
FT	DISULFID	2161	2313	BY SIMILARITY.	(BY SIMILARITY).
FT	CARBOHYD	61	61	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	233	233	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	259	259	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	423	423	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	601	601	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	880	880	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	958	958	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	1015	1015	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	1022	1022	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	1026	1026	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	1044	1044	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	1076	1076	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	1087	1087	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	1136	1136	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	1161	1161	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	1192	1192	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	1255	1255	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	1268	1268	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	1273	1273	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	1274	1274	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	1302	1302	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	1316	1316	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	1340	1340	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	1378	1378	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	1797	1797	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	2105	2105	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	2105	2105	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	SEQUENCE	2319 AA;	2566148 MW;	FD054DBE051DB2A01 CRC64;	
QY	Query Match	86.3%;	Score 752;	DB 1; Length 2319;	
Dd	Best Local Similarity	84.1%;	Pred. No. 1.3e-64;		
Dd	Matches 138;	Conservative 11;	Mismatches 15;	Indels 0; Gaps 0;	
Qy	1 CDLNSCSPLGMSKAISSDAQTASSYFTNNFATSPSKAPLHLQGRSNWRPQVNPKE 60				
Dd	2156 CDLNSCSPILGMSKVISDTQITASSYFTNMFAWPSQARLHQLQRTNWRPQNDPKQ 2215				
Qy	61 WLQVDFOQTKMKTGTTCGVKSLLTSVMVKFEFLISSODGHQWTLFPQNGKVKVPQGNQD 120				
Dd	2216 WLQVDLQTKMKVTGIITQGVKSLLTSFMVKFEFLISSODGHHTWTQILYNGKVKVPQGNQD 2275				
Qy	121 STTPVNSLDPELLTRYLRIRHQSWVHOIALRMEVLGCEAQDLY 164				
Dd	2276 STTPPMNSLDPELLTRYLRIRHQIWEHOIALRLLELTGCEAAQQY 2319				

```

RESULT 3
FAS_PIG
ID_FAS_PIG STANDARD; PRT; 2133 AA.
AC P12763; Q95243;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Coagulation factor VIII precursor (Procoagulant component).
GN F8 OR C8.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Healey J.F., Lubin I.M., Lollar P.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 705-1573 FROM N.A.
RA MEDLINE=86287369; PubMed=3016730;
RA Toole J.J., Pittman D.D., Orr E.C., Murtha P., Wasley L.C.,
RA Kaufman R.J.;
RT "A large region (approximately equal to 95 kDa) of human factor VIII
RL is dispensable for in vitro procoagulant activity.";
RN [3]
RP SEQUENCE OF 392-759 FROM N.A.
RA MEDLINE=94179260; PubMed=7510693;
RA Lubin I.M., Healey J.F., Scandella D., Runge M.S., Lollar P.;
RT "Elimination of a major inhibitor epitope in factor VIII.";
RL J. Biol. Chem. 269:8639-8641(1994).
CC -!- FUNCTION: Factor VIII, along with calcium and phospholipid, acts
CC as a cofactor for factor IXa when it converts factor X to the
CC activated form, factor Xa.
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- SIMILARITY: Contains 3 F5/8 type A domains.
CC -!- SIMILARITY: Contains 2 F5/8 type C domains.
CC -!- SIMILARITY: STRONG, TO COAGULATION FACTOR V.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announcement/
CC or send an email to license@isb-sib.ch).
CC
-----
EMBL; U49517; AAB06705.1; -
DR PIR; A25945; A25945.
DR PIR; T42763; T42763.
DR HSP; P00451; 1CFG.
DR InterPro; IPR001117; Cu-oxidase.
DR InterPro; IPR008972; Cupredoxin.
DR InterPro; IPR000421; FAS8_C.
DR InterPro; IPR008979; Gal_Bind_like.
DR Pfam; PF00394; Cu-oxidase; 3.
DR Pfam; PF00754; F5_F8 type C; 2.
DR SMART; SM00231; FAS8C_2.
DR PROSITE; PS01285; FAS8C_1; 2.
DR PROSITE; PS01286; FAS8C_2.
DR PROSITE; PS00022; FAS8C_3; 2.
DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; 3.
KW Blood coagulation; Repeat; Plasma; Acute phase; Calcium;
KW Signal; Glycoprotein; Sulfation.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 2133 COAGULATION FACTOR VIII.
FT DOMAIN 20 357 F5/8 TYPE A 1.
FT DOMAIN 20 199 PLASTOCYANIN-LIKE 1.
FT DOMAIN 207 357 PLASTOCYANIN-LIKE 2.
FT DOMAIN 399 730 F5/8 TYPE A 2.
FT DOMAIN 399 573 PLASTOCYANIN-LIKE 3.

```

```

FT DOMAIN 583 730 PLASTOCYANIN-LIKE 4.
FT DOMAIN 760 1599 B.
FT DOMAIN 1495 1822 F5/8 TYPE A 3.
FT DOMAIN 1495 1659 PLASTOCYANIN-LIKE 5.
FT DOMAIN 1669 1822 PLASTOCYANIN-LIKE 6.
FT DOMAIN 1822 1970 F5/8 TYPE C 1.
FT DOMAIN 1975 2127 F5/8 TYPE C 2.
FT SITE 391 392 CLEAVAGE (BY THROMBIN) (BY SIMILARITY).
FT SITE 759 760 CLEAVAGE (BY THROMBIN) (BY SIMILARITY).
FT SITE 1449 1450 CLEAVAGE (ACTIVATION) (BY SIMILARITY).
FT MOD_RES 737 737 CLEAVAGE (BY THROMBIN) (BY SIMILARITY).
FT MOD_RES 738 738 CLEAVAGE (BY THROMBIN) (BY SIMILARITY).
FT MOD_RES 742 742 SULFATION (BY SIMILARITY).
FT DISULFID 173 199 SULFATION (BY SIMILARITY).
FT DISULFID 547 573 PROBABLE.
FT DISULFID 1633 1659 PROBABLE.
FT DISULFID 1822 1970 BY SIMILARITY.
FT DISULFID 1975 2127 BY SIMILARITY.
FT CARBOHYD 233 233 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 259 259 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 601 601 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 929 929 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 985 985 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 1025 1025 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 1111 1111 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 1181 1181 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 1208 1208 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 1245 1245 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 1265 1265 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 1335 1335 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 1408 1408 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 1611 1611 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 1919 1919 N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 713 734 N -> M (IN REF. 2).
FT CONFLICT 734 734 I -> T (IN REF. 2).
FT CONFLICT 792 792 G -> Q (IN REF. 2).
FT CONFLICT 1133 1133 E -> F (IN REF. 2).
FT CONFLICT 1191 1191 I -> L (IN REF. 2).
FT CONFLICT 1209 1209 R -> F (IN REF. 2).
FT CONFLICT 1437 1437 C -> G (IN REF. 2).
FT CONFLICT 1456 1456 F -> R (IN REF. 2).
FT CONFLICT 1539 1539 F -> R (IN REF. 2).
FT CONFLICT 1546 1546 Q -> N (IN REF. 2).
SQ SEQUENCE 2133 AA; 239304 MW; 152BBA8997F570DA CRC64;

Query Match 82.7%; Score 720; DB 1; Length 2133;
Best Local Similarity 79.9%; Pred. No. 1.5e-61;
Matches 131; Conservative 20; Mismatches 13; Indels 0; Gaps 0;

QY 1 CDLNSCSMPGLGSKAISDAQITASSYFTNMTWATNPSKARLHLQGRSNARVQVNPKE 60
Db 1970 CDLNSCSMPGLGSKAISDSQITASSHLNIFATWSPSQARLHLQGRTNARVSSAE 2029

QY 61 WLQYDFCKTKVTKVGTITQGVKSLTSMYKVFISSSQDCHOWTLFFQNGKVKVFGNQD 120
Db 2030 WLQYDLQTKVTKVGTITQGVKSLTSMYKVFISSSQDGRWTLFLQDGHKVKVFGNQD 2089

QY 121 SFTFVNSLDPPLLTLYRLRHPOSWTHQIALRMEVLGCCEAQQLY 164
Db 2090 SFTFVNSLDPPLLTLYRLRHPOSWTHQIALRMEVLGCCEAQQLY 2133

RESULT 4
FAS_PIG STANDARD; PRT; 2258 AA.
AC Q9GLEP1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Coagulation factor V precursor (Activated protein C cofactor).
GN F5.
OS Sus scrofa (Pig).

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A., AND 3D-STRUCTURE MODELING OF F5/8 TYPE A AND C
 RP DOMAINS.
 RC TISSUE=Liver;
 RX MEDLINE=21121490; PubMed=11229814;
 RA Grimm D.R., Colter M.B., Braunschweig M., Alexander L.J., Neame P.J.,
 RA Kim H.K.W.;
 RT "Porcine factor V: cDNA cloning, gene mapping, three-dimensional
 RT protein modeling of membrane binding sites and comparative anatomy of
 RL domains";
 RL Cell. Mol. Life Sci. 58:148-159(2001).
 CC -!- FUNCTION: Coagulation factor V is a cofactor that participates
 CC with factor Xa to activate prothrombin to thrombin.
 CC -!- SUBUNIT: Factor Va is composed of a heavy chain and a light
 CC chain, noncovalently bound. The interaction between the two chains
 CC is calcium-dependent.
 CC -!- DOMAIN: Domain B contains 41 X 9 AA tandem repeats. Domains C1
 CC and C2 may be involved in membrane binding.
 CC -!- PTM: Thrombin activates factor V proteolytically to the active
 CC cofactor, factor Va (formation of a heavy chain at the N-
 CC terminus and a light chain at the C-terminus).
 CC -!- SIMILARITY: Contains 3 F5/8 type A domains.
 CC -!- SIMILARITY: Contains 2 F5/8 type C domains.
 CC -!- SIMILARITY: STRONG, TO COAGULATION FACTOR VIII.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AF191308; AAC28331.1; --
 DR HSPF; P12259, 1CZT.
 DR InterPro; IPR001117; Cu-oxidase.
 DR InterPro; IPR008972; Cupredoxin.
 DR InterPro; IPR0040421; FAS8_C.
 DR InterPro; IPR008979; Gal Bind_like.
 DR Pfam; PF003194; Cu-oxidase; 3.
 DR Pfam; PF00754; F5 F8 type_C; 2.
 DR SMART; SM00231; FAS8C; 2.
 DR PROSITE; PS01285; FAS8C_1; 2.
 DR PROSITE; PS01286; FAS8C_2; 2.
 DR PROSITE; PS00022; FAS8C_3; 2.
 DR PROSITE; PS00079; MULTICOPPER OXIDASE1; 2.
 DR Blood coagulation; Glycoprotein; Sulfation; Calcium; Signal; Zymogen;
 KW Repeat.
 FT SIGNAL. 1 22 POTENTIAL.
 FT CHAIN 23 2258 COAGULATION FACTOR V.
 FT CHAIN 23 737 COAGULATION FACTOR V HEAVY CHAIN (BY
 FT (BY SIMILARITY).
 FT PROPEP 738 1611 ACTIVATION PEPTIDE (CONNECTING REGION)
 FT (BY SIMILARITY).
 FT CHAIN 1612 2258 COAGULATION FACTOR V LIGHT CHAIN (BY
 FT (BY SIMILARITY).
 FT DOMAIN 30 329 F5/8 TYPE A 1.
 FT DOMAIN 30 193 PLASTOCYANIN-LIKE 1.
 FT DOMAIN 203 329 PLASTOCYANIN-LIKE 2.
 FT DOMAIN 348 683 F5/8 TYPE A 2.
 FT DOMAIN 348 525 PLASTOCYANIN-LIKE 3.
 FT DOMAIN 535 683 PLASTOCYANIN-LIKE 4.
 FT DOMAIN 621 1611 B.
 FT DOMAIN 1168 1539 41 X 9 AA APPROXIMATE TANDEM REPEATS OF
 FT T-L-S-P-D-L-[GS]-[HQ]-T.
 FT REPEAT 1168 1176 1.
 FT REPEAT 1177 1185 2.
 FT REPEAT 1186 1194 3.
 FT REPEAT 1195 1203 4.
 FT REPEAT 1204 1212 5.

92 1213 1221
 93 REPEAT 1222
 94 REPEAT 1230
 95 REPEAT 1231
 96 REPEAT 1239
 97 REPEAT 1240
 98 REPEAT 1248
 99 REPEAT 1249
 100 REPEAT 1257
 101 REPEAT 1258
 102 REPEAT 1266
 103 REPEAT 1267
 104 REPEAT 1275
 105 REPEAT 1276
 106 REPEAT 1284
 107 REPEAT 1285
 108 REPEAT 1293
 109 REPEAT 1302
 110 REPEAT 1303
 111 REPEAT 1311
 112 REPEAT 1312
 113 REPEAT 1320
 114 REPEAT 1321
 115 REPEAT 1329
 116 REPEAT 1330
 117 REPEAT 1338
 118 REPEAT 1347
 119 REPEAT 1348
 120 REPEAT 1356
 121 REPEAT 1357
 122 REPEAT 1365
 123 REPEAT 1374
 124 REPEAT 1375
 125 REPEAT 1383
 126 REPEAT 1392
 127 REPEAT 1401
 128 REPEAT 1402
 129 REPEAT 1410
 130 REPEAT 1411
 131 REPEAT 1419
 132 REPEAT 1420
 133 REPEAT 1428
 134 REPEAT 1437
 135 REPEAT 1438
 136 REPEAT 1446
 137 REPEAT 1447
 138 REPEAT 1455
 139 REPEAT 1456
 140 REPEAT 1464
 141 REPEAT 1465
 142 REPEAT 1473
 143 REPEAT 1474
 144 REPEAT 1482
 145 REPEAT 1483
 146 REPEAT 1491
 147 REPEAT 1492
 148 REPEAT 1500
 149 REPEAT 1501
 150 REPEAT 1509
 151 REPEAT 1510
 152 REPEAT 1518
 153 REPEAT 1519
 154 REPEAT 1527
 155 REPEAT 1531
 156 REPEAT 1539
 157 REPEAT 1616
 158 REPEAT 1616
 159 REPEAT 1616
 160 REPEAT 1616
 161 REPEAT 1616
 162 REPEAT 1616
 163 REPEAT 1616
 164 REPEAT 1616
 165 REPEAT 1616
 166 REPEAT 1616
 167 REPEAT 1616
 168 REPEAT 1616
 169 REPEAT 1616
 170 REPEAT 1616
 171 REPEAT 1616
 172 REPEAT 1616
 173 REPEAT 1616
 174 REPEAT 1616
 175 REPEAT 1616
 176 REPEAT 1616
 177 REPEAT 1616
 178 REPEAT 1616
 179 REPEAT 1616
 180 REPEAT 1616
 181 REPEAT 1616
 182 REPEAT 1616
 183 REPEAT 1616
 184 REPEAT 1616
 185 REPEAT 1616
 186 REPEAT 1616
 187 REPEAT 1616
 188 REPEAT 1616
 189 REPEAT 1616
 190 REPEAT 1616
 191 REPEAT 1616
 192 REPEAT 1616
 193 REPEAT 1616
 194 REPEAT 1616
 195 REPEAT 1616
 196 REPEAT 1616
 197 REPEAT 1616
 198 REPEAT 1616
 199 REPEAT 1616
 200 REPEAT 1616
 201 REPEAT 1616
 202 REPEAT 1616
 203 REPEAT 1616
 204 REPEAT 1616
 205 REPEAT 1616
 206 REPEAT 1616
 207 REPEAT 1616
 208 REPEAT 1616
 209 REPEAT 1616
 210 REPEAT 1616
 211 REPEAT 1616
 212 REPEAT 1616
 213 REPEAT 1616
 214 REPEAT 1616
 215 REPEAT 1616
 216 REPEAT 1616
 217 REPEAT 1616
 218 REPEAT 1616
 219 REPEAT 1616
 220 REPEAT 1616
 221 REPEAT 1616
 222 REPEAT 1616
 223 REPEAT 1616
 224 REPEAT 1616
 225 REPEAT 1616
 226 REPEAT 1616
 227 REPEAT 1616
 228 REPEAT 1616
 229 REPEAT 1616
 230 REPEAT 1616
 231 REPEAT 1616
 232 REPEAT 1616
 233 REPEAT 1616
 234 REPEAT 1616
 235 REPEAT 1616
 236 REPEAT 1616
 237 REPEAT 1616
 238 REPEAT 1616
 239 REPEAT 1616
 240 REPEAT 1616
 241 REPEAT 1616
 242 REPEAT 1616
 243 REPEAT 1616
 244 REPEAT 1616
 245 REPEAT 1616
 246 REPEAT 1616
 247 REPEAT 1616
 248 REPEAT 1616
 249 REPEAT 1616
 250 REPEAT 1616
 251 REPEAT 1616
 252 REPEAT 1616
 253 REPEAT 1616
 254 REPEAT 1616
 255 REPEAT 1616
 256 REPEAT 1616
 257 REPEAT 1616
 258 REPEAT 1616
 259 REPEAT 1616
 260 REPEAT 1616
 261 REPEAT 1616
 262 REPEAT 1616
 263 REPEAT 1616
 264 REPEAT 1616
 265 REPEAT 1616
 266 REPEAT 1616
 267 REPEAT 1616
 268 REPEAT 1616
 269 REPEAT 1616
 270 REPEAT 1616
 271 REPEAT 1616
 272 REPEAT 1616
 273 REPEAT 1616
 274 REPEAT 1616
 275 REPEAT 1616
 276 REPEAT 1616
 277 REPEAT 1616
 278 REPEAT 1616
 279 REPEAT 1616
 280 REPEAT 1616
 281 REPEAT 1616
 282 REPEAT 1616
 283 REPEAT 1616
 284 REPEAT 1616
 285 REPEAT 1616
 286 REPEAT 1616
 287 REPEAT 1616
 288 REPEAT 1616
 289 REPEAT 1616
 290 REPEAT 1616
 291 REPEAT 1616
 292 REPEAT 1616
 293 REPEAT 1616
 294 REPEAT 1616
 295 REPEAT 1616
 296 REPEAT 1616
 297 REPEAT 1616
 298 REPEAT 1616
 299 REPEAT 1616
 300 REPEAT 1616
 301 REPEAT 1616
 302 REPEAT 1616
 303 REPEAT 1616
 304 REPEAT 1616
 305 REPEAT 1616
 306 REPEAT 1616
 307 REPEAT 1616
 308 REPEAT 1616
 309 REPEAT 1616
 310 REPEAT 1616
 311 REPEAT 1616
 312 REPEAT 1616
 313 REPEAT 1616
 314 REPEAT 1616
 315 REPEAT 1616
 316 REPEAT 1616
 317 REPEAT 1616
 318 REPEAT 1616
 319 REPEAT 1616
 320 REPEAT 1616
 321 REPEAT 1616
 322 REPEAT 1616
 323 REPEAT 1616
 324 REPEAT 1616
 325 REPEAT 1616
 326 REPEAT 1616
 327 REPEAT 1616
 328 REPEAT 1616
 329 REPEAT 1616
 330 REPEAT 1616
 331 REPEAT 1616
 332 REPEAT 1616
 333 REPEAT 1616
 334 REPEAT 1616
 335 REPEAT 1616
 336 REPEAT 1616
 337 REPEAT 1616
 338 REPEAT 1616
 339 REPEAT 1616
 340 REPEAT 1616
 341 REPEAT 1616
 342 REPEAT 1616
 343 REPEAT 1616
 344 REPEAT 1616
 345 REPEAT 1616
 346 REPEAT 1616
 347 REPEAT 1616
 348 REPEAT 1616
 349 REPEAT 1616
 350 REPEAT 1616
 351 REPEAT 1616
 352 REPEAT 1616
 353 REPEAT 1616
 354 REPEAT 1616
 355 REPEAT 1616
 356 REPEAT 1616
 357 REPEAT 1616
 358 REPEAT 1616
 359 REPEAT 1616
 360 REPEAT 1616
 361 REPEAT 1616
 362 REPEAT 1616
 363 REPEAT 1616
 364 REPEAT 1616
 365 REPEAT 1616
 366 REPEAT 1616
 367 REPEAT 1616
 368 REPEAT 1616
 369 REPEAT 1616
 370 REPEAT 1616
 371 REPEAT 1616
 372 REPEAT 1616
 373 REPEAT 1616
 374 REPEAT 1616
 375 REPEAT 1616
 376 REPEAT 1616
 377 REPEAT 1616
 378 REPEAT 1616
 379 REPEAT 1616
 380 REPEAT 1616
 381 REPEAT 1616
 382 REPEAT 1616
 383 REPEAT 1616
 384 REPEAT 1616
 385 REPEAT 1616
 386 REPEAT 1616
 387 REPEAT 1616
 388 REPEAT 1616
 389 REPEAT 1616
 390 REPEAT 1616
 391 REPEAT 1616
 392 REPEAT 1616
 393 REPEAT 1616
 394 REPEAT 1616
 395 REPEAT 1616
 396 REPEAT 1616
 397 REPEAT 1616
 398 REPEAT 1616
 399 REPEAT 1616
 400 REPEAT 1616
 401 REPEAT 1616
 402 REPEAT 1616
 403 REPEAT 1616
 404 REPEAT 1616
 405 REPEAT 1616
 406 REPEAT 1616
 407 REPEAT 1616
 408 REPEAT 1616
 409 REPEAT 1616
 410 REPEAT 1616
 411 REPEAT 1616
 412 REPEAT 1616
 413 REPEAT 1616
 414 REPEAT 1616
 415 REPEAT 1616
 416 REPEAT 1616
 417 REPEAT 1616
 418 REPEAT 1616
 419 REPEAT 1616
 420 REPEAT 1616
 421 REPEAT 1616
 422 REPEAT 1616
 423 REPEAT 1616
 424 REPEAT 1616
 425 REPEAT 1616
 426 REPEAT 1616
 427 REPEAT 1616
 428 REPEAT 1616
 429 REPEAT 1616
 430 REPEAT 1616
 431 REPEAT 1616
 432 REPEAT 1616
 433 REPEAT 1616
 434 REPEAT 1616
 435 REPEAT 1616
 436 REPEAT 1616
 437 REPEAT 1616
 438 REPEAT 1616
 439 REPEAT 1616
 440 REPEAT 1616
 441 REPEAT 1616
 442 REPEAT 1616
 443 REPEAT 1616
 444 REPEAT 1616
 445 REPEAT 1616
 446 REPEAT 1616
 447 REPEAT 1616
 448 REPEAT 1616
 449 REPEAT 1616
 450 REPEAT 1616
 451 REPEAT 1616
 452 REPEAT 1616
 453 REPEAT 1616
 454 REPEAT 1616
 455 REPEAT 1616
 456 REPEAT 1616
 457 REPEAT 1616
 458 REPEAT 1616
 459 REPEAT 1616
 460 REPEAT 1616
 461 REPEAT 1616
 462 REPEAT 1616
 463 REPEAT 1616
 464 REPEAT 1616
 465 REPEAT 1616
 466 REPEAT 1616
 467 REPEAT 1616
 468 REPEAT 1616
 469 REPEAT 1616
 470 REPEAT 1616
 471 REPEAT 1616
 472 REPEAT 1616
 473 REPEAT 1616
 474 REPEAT 1616
 475 REPEAT 1616
 476 REPEAT 1616
 477 REPEAT 1616
 478 REPEAT 1616
 479 REPEAT 1616
 480 REPEAT 1616
 481 REPEAT 1616
 482 REPEAT 1616
 483 REPEAT 1616
 484 REPEAT 1616
 485 REPEAT 1616
 486 REPEAT 1616
 487 REPEAT 1616
 488 REPEAT 1616
 489 REPEAT 1616
 490 REPEAT 1616
 491 REPEAT 1616
 492 REPEAT 1616
 493 REPEAT 1616
 494 REPEAT 1616
 495 REPEAT 1616
 496 REPEAT 1616
 497 REPEAT 1616
 498 REPEAT 1616
 499 REPEAT 1616
 500 REPEAT 1616
 501 REPEAT 1616
 502 REPEAT 1616
 503 REPEAT 1616
 504 REPEAT 1616
 505 REPEAT 1616
 506 REPEAT 1616
 507 REPEAT 1616
 508 REPEAT 1616
 509 REPEAT 1616
 510 REPEAT 1616
 511 REPEAT 1616
 512 REPEAT 1616
 513 REPEAT 1616
 514 REPEAT 1616
 515 REPEAT 1616
 516 REPEAT 1616
 517 REPEAT 1616
 518 REPEAT 1616
 519 REPEAT 1616
 520 REPEAT 1616
 521 REPEAT 1616
 522 REPEAT 1616
 523 REPEAT 1616
 524 REPEAT 1616
 525 REPEAT 1616
 526 REPEAT 1616
 527 REPEAT 1616
 528 REPEAT 1616
 529 REPEAT 1616
 530 REPEAT 1616
 531 REPEAT 1616
 532 REPEAT 1616
 533 REPEAT 1616
 534 REPEAT 1616
 535 REPEAT 1616
 536 REPEAT 1616
 537 REPEAT 1616
 538 REPEAT 1616
 539 REPEAT 1616
 540 REPEAT 1616
 541 REPEAT 1616
 542 REPEAT 1616
 543 REPEAT 1616
 544 REPEAT 1616
 545 REPEAT 1616
 546 REPEAT 1616
 547 REPEAT 1616
 548 REPEAT 1616
 549 REPEAT 1616
 550 REPEAT 1616
 551 REPEAT 1616
 552 REPEAT 1616
 553 REPEAT 1616
 554 REPEAT 1616
 555 REPEAT 1616
 556 REPEAT 1616
 557 REPEAT 1616
 558 REPEAT 1616
 559 REPEAT 1616
 560 REPEAT 1616
 561 REPEAT 1616
 562 REPEAT 1616
 563 REPEAT 1616
 564 REPEAT 1616
 565 REPEAT 1616
 566 REPEAT 1616
 567 REPEAT 1616
 568 REPEAT 1616
 569 REPEAT 1616
 570 REPEAT 1616
 571 REPEAT 1616
 572 REPEAT 1616
 573 REPEAT 1616
 574 REPEAT 1616
 575 REPEAT 1616
 576 REPEAT 1616
 577 REPEAT 1616
 578 REPEAT 1616
 579 REPEAT 1616
 580 REPEAT 1616
 581 REPEAT 1616
 582 REPEAT 1616
 583 REPEAT 1616
 584 REPEAT 1616
 585 REPEAT 1616
 586 REPEAT 1616
 587 REPEAT 1616
 588 REPEAT 1616
 589 REPEAT 1616
 590 REPEAT 1616
 591 REPEAT 1616
 592 REPEAT 1616
 593 REPEAT 1616
 594 REPEAT 1616
 595 REPEAT 1616
 596 REPEAT 1616
 597 REPEAT 1616
 598 REPEAT 1616
 599 REPEAT 1616
 600 REPEAT 1616
 601 REPEAT 1616
 602 REPEAT 1616
 603 REPEAT 1616
 604 REPEAT 1616
 605 REPEAT 1616
 606 REPEAT 1616
 607 REPEAT 1616
 608 REPEAT 1616
 609 REPEAT 1616
 610 REPEAT 1616
 611 REPEAT 1616
 612 REPEAT 1616
 613 REPEAT 1616
 614 REPEAT 1616
 615 REPEAT 1616
 616 REPEAT 1616
 617 REPEAT 1616
 618 REPEAT 1616
 619 REPEAT 1616
 620 REPEAT 1616
 621 REPEAT 1616
 622 REPEAT 1616
 623 REPEAT 1616
 624 REPEAT 1616
 625 REPEAT 1616
 626 REPEAT 1616
 627 REPEAT 1616
 628 REPEAT 1616
 629 REPEAT 1616
 630 REPEAT 1616
 631 REPEAT 1616
 632 REPEAT 1616
 633 REPEAT 1616
 634 REPEAT 1616
 635 REPEAT 1616
 636 REPEAT 1616
 637 REPEAT 1616
 638 REPEAT 1616
 639 REPEAT 1616
 640 REPEAT 1616
 641 REPEAT 1616
 642 REPEAT 1616
 643 REPEAT 1616
 644 REPEAT 1616
 645 REPEAT 1616
 646 REPEAT 1616
 647 REPEAT 1616
 648 REPEAT 1616
 649 REPEAT 1616
 650 REPEAT 1616
 651 REPEAT 1616
 652 REPEAT 1616
 653 REPEAT 1616
 654 REPEAT 1616
 655 REPEAT 1616
 656 REPEAT 1616
 657 REPEAT 1616
 658 REPEAT 1616
 659 REPEAT 1616
 660 REPEAT 1616
 661 REPEAT 1616
 662 REPEAT 1616
 663 REPEAT 1616
 664 REPEAT 1616
 665 REPEAT 1616
 666 REPEAT 1616
 667 REPEAT 1616
 668 REPEAT 1616
 669 REPEAT 1616
 670 REPEAT 1616
 671 REPEAT 1616
 672 REPEAT 1616
 673 REPEAT 1616
 674 REPEAT 1616
 675 REPEAT 1616
 676 REPEAT 1616
 677 REPEAT 1616
 678 REPEAT 1616
 679 REPEAT 1616
 680 REPEAT 1616
 681 REPEAT 1616
 682 REPEAT 1616
 683 REPEAT 1616
 684 REPEAT 1616
 685 REPEAT 1616
 686 REPEAT 1616
 687 REPEAT 1616
 688 REPEAT 1616
 689 REPEAT 1616
 690 REPEAT 1616
 691 REPEAT 1616
 692 REPEAT 1616
 693 REPEAT 1616
 694 REPEAT 1616
 695 REPEAT 1616
 696 REPEAT 1616
 697 REPEAT 1616
 698 REPEAT 1616
 699 REPEAT 1616
 700 REPEAT 1616
 701 REPEAT 1616
 702 REPEAT 1616
 703 REPEAT 1616
 704 REPEAT 1616
 705 REPEAT 1616
 706 REPEAT 1616
 707 REPEAT 1616
 708 REPEAT 1616
 709 REPEAT 1616
 710 REPEAT 1616
 711 REPEAT 1616
 712 REPEAT 1616
 713 REPEAT 1616
 714 REPEAT 1616
 715 REPEAT 1616
 716 REPEAT 1616
 717 REPEAT 1616
 718 REPEAT 1616
 719 REPEAT 1616
 720 REPEAT 1616
 721 REPEAT 1616
 722 REPEAT 1616
 723 REPEAT 1616
 724 REPEAT 1616
 725 REPEAT 1616
 726 REPEAT 1616
 727 REPEAT 1616
 728 REPEAT 1616
 729 REPEAT 1616
 730 REPEAT 1616
 731 REPEAT 1616
 732 REPEAT 1616
 733 REPEAT 1616
 734 REPEAT 1616
 735 REPEAT 1616
 736 REPEAT 1616
 737 REPEAT 1616
 738 REPEAT 1616
 739 REPEAT 1616
 740 REPEAT 1616
 741 REPEAT 1616
 742 REPEAT 1616
 743 REPEAT 1616
 744 REPEAT 1616
 745 REPEAT 1616
 746 REPEAT 1616
 747 REPEAT 1616
 748 REPEAT 1616
 749 REPEAT 1616
 750 REPEAT 1616
 751 REPEAT 1616
 752 REPEAT 1616
 753 REPEAT 1616
 754 REPEAT 1616
 755 REPEAT 1616
 756 REPEAT 1616
 757 REPEAT 1616
 758 REPEAT 1616
 759 REPEAT 1616
 760 REPEAT 1616
 761 REPEAT 1616
 762 REPEAT 1616
 763 REPEAT 1616
 764 REPEAT 1616
 765 REPEAT 1616
 766 REPEAT 1616
 767 REPEAT 1616
 768 REPEAT 1616
 769 REPEAT 1616
 770 REPEAT 1616
 771 REPEAT 1616
 772 REPEAT 1616
 773 REPEAT 1616
 774 REPEAT 1616
 775 REPEAT 1616
 776 REPEAT 1616
 777 REPEAT 1616
 778 REPEAT 1616
 779 REPEAT 1616
 780 REPEAT 1616
 781 REPEAT 1616
 782 REPEAT 1616
 783 REPEAT 1616
 784 REPEAT 1616
 785 REPEAT 1616
 786 REPEAT 1616
 787 REPEAT 1616
 788 REPEAT 1616
 789 REPEAT 1616
 790 REPEAT 1616
 791 REPEAT 1616
 792 REPEAT 1616
 793 REPEAT 1616
 794 REPEAT 1616
 795 REPEAT 1616
 796 REPEAT 1616
 797 REPEAT 1616
 798 REPEAT 1616
 799 REPEAT 1616
 800 REPEAT 1616
 801 REPEAT 1616
 802 REPEAT

```

FT CARBOHYD 741 741 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 752 752 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 760 760 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 776 776 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 782 782 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 899 899 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 960 960 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1048 1048 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1057 1057 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1066 1066 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1073 1073 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1089 1089 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1174 1174 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1480 1480 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1537 1537 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1597 1597 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1737 1737 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1886 1886 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2044 2044 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2243 2243 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 2258 AA; 256078 MW; 9159B9E0076A2ACC CRC64;

Query Match 44.2%; Score 385; DB 1; Length 2258;
Best Local Similarity 44.3%; Pred. No. 5e-29;
Matches 74; Conservative 33; Mismatches 54; Indels 6; Gaps 3;

QY 1 CDLNSCMELGMSKAIISDAQITASSYFTNMFAT-WSPSKARLHLOGRSNWAPQVNP 59
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2095 CEVNGCSTPLGMEGNIKEOITASSPKKSGWGDYWEFFRRLNAQGRVNAQAKANN 2154
QY 60 EWLQVDFQKTMKGVITQGVKLLTSYKFEFLISSQDGHQWTLFFQNGKV--KVFOG 117
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2155 QWLQIDLKIKKITAITTCGCKSLSESEWYKRYTIOYSDRGVSKSVREKSNVVDKIFEG 2214
QY 118 NQDSFTPVNSLDPLTLRLVLRHPQSVHQAIRMEVLGCEAODLY 164
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2215 NNKIGHVKNFFNPPIIRIFIRIPKMNQSIARLELFGC---DIY 2258

RESULT 5
FAS_BOVIN STANDARD; PRT; 2211 AA.
AC Q28107; Q28108;
AT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Coagulation factor V precursor (Activated protein C cofactor).
GN F5.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=92147638; PubMed=1737753;
RA Guinco E.R., Emon C.T., Mann K.G., Macgillivray R.T.;
RT "The complete cDNA sequence of bovine coagulation factor V.";
RL J. Biol. Chem. 267:2971-2978(1992).
RN [2]
RP DISULFIDE BONDS.
RX MEDLINE=95034740; PubMed=7947716;
RA Xue J., Kalafatis M., Silvera J.R., Kung C., Mann K.G.;
RT "Determination of the disulfide bridges in factor Va heavy chain.";
RL Biochemistry 33:13109-13116(1994).
CC -1- FUNCTION: Coagulation factor V is a cofactor that participates
CC with factor Xa to activate prothrombin to thrombin.
CC -1- SUBUNIT: Factor Va is composed of a heavy chain and a light
CC chain, noncovalently bound. The interaction between the two chains
CC is calcium-dependent.
CC -1- DOMAIN: Domain B contains 29.5 X 9 AA tandem repeats, and 2 X 14
CC AA repeats.

```

```

CC -1- PTM: Thrombin activates factor V proteolytically to the active
CC cofactor, factor Va (formation of a heavy chain at the N-
CC terminus and a light chain at the C-terminus).
CC -1- PTM: Sulfation is required for efficient thrombin cleavage and
CC activation and for full procoagulant activity (By similarity).
CC -1- SIMILARITY: Contains 3 F5/8 type A domains.
CC -1- SIMILARITY: Contains 2 F5/8 type C domains.
CC -1- SIMILARITY: STRONG, TO COAGULATION FACTOR VIII.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch)
CC -----
CC EMBL; M81440; AAA30512.1; .
CC EMBL; M81441; AAA30513.1; .
CC PIR; A42580; KFBOS.
CC HSP; P12259; ICZT.
CC InterPro; IPR001117; Cu-oxidase.
CC InterPro; IPR008972; Cupredoxin.
CC InterPro; IPR000421; F58C.
CC InterPro; IPR008979; Gal_bind_like.
CC Pfam; PF00394; Cu-oxidase; 3.
CC Pfam; PF00754; F5_F8_type_C; 2.
CC SMART; SM00231; F58C; 2.
CC PROSITE; PS01285; F58C_1; 2.
CC PROSITE; PS01286; F58C_2; 2.
CC PROSITE; PS00022; F58C_3; 2.
CC PROSITE; PS00079; MULTICOPPER_OXIDASE1; 2.
KW Blood coagulation; Glycoprotein; Sulfation; Calcium; Signal; Zymogen;
KW Repeat.
FT SIGNAL 1 28
FT CHAIN 29 2211
FT CHAIN 29 741
FT PROPEP 742 1564
FT CHAIN 1565 2211
FT CHAIN 30 327
FT DOMAIN 30 193
FT DOMAIN 203 327
FT DOMAIN 348 686
FT DOMAIN 348 525
FT DOMAIN 535 686
FT DOMAIN 696 1564
FT DOMAIN 1124 1151
FT DOMAIN 1124 1137
FT REPEAT 1138 1151
FT DOMAIN 1188 1453
FT REPEAT 1188 1196
FT REPEAT 1197 1205
FT REPEAT 1206 1214
FT REPEAT 1215 1223
FT REPEAT 1224 1232
FT REPEAT 1233 1241
FT REPEAT 1242 1250
FT REPEAT 1251 1259
FT REPEAT 1260 1268
FT REPEAT 1269 1277
FT REPEAT 1278 1286
FT REPEAT 1287 1295
FT REPEAT 1296 1304
FT REPEAT 1305 1313
FT REPEAT 1314 1322
FT REPEAT 1323 1331
FT REPEAT 1332 1340
FT REPEAT 1341 1349
FT REPEAT 1350 1358
FT REPEAT 2-1.
FT REPEAT 2-2.
FT REPEAT 2-3.
FT REPEAT 2-4.
FT REPEAT 2-5.
FT REPEAT 2-6.
FT REPEAT 2-7.
FT REPEAT 2-8.
FT REPEAT 2-9.
FT REPEAT 2-10.
FT REPEAT 2-11.
FT REPEAT 2-12.
FT REPEAT 2-13.
FT REPEAT 2-14.
FT REPEAT 2-15.
FT REPEAT 2-16.
FT REPEAT 2-17.
FT REPEAT 2-18.
FT REPEAT 2-19.
FT REPEAT 2-20.
FT REPEAT 2-21.
FT REPEAT 2-22.
FT REPEAT 2-23.
FT REPEAT 2-24.
FT REPEAT 2-25.
FT REPEAT 2-26.
FT REPEAT 2-27.
FT REPEAT 2-28.
FT REPEAT 2-29.
FT REPEAT 2-30.
FT REPEAT 2-31.
FT REPEAT 2-32.
FT REPEAT 2-33.
FT REPEAT 2-34.
FT REPEAT 2-35.
FT REPEAT 2-36.
FT REPEAT 2-37.
FT REPEAT 2-38.
FT REPEAT 2-39.
FT REPEAT 2-40.
FT REPEAT 2-41.
FT REPEAT 2-42.
FT REPEAT 2-43.
FT REPEAT 2-44.
FT REPEAT 2-45.
FT REPEAT 2-46.
FT REPEAT 2-47.
FT REPEAT 2-48.
FT REPEAT 2-49.
FT REPEAT 2-50.
FT REPEAT 2-51.
FT REPEAT 2-52.
FT REPEAT 2-53.
FT REPEAT 2-54.
FT REPEAT 2-55.
FT REPEAT 2-56.
FT REPEAT 2-57.
FT REPEAT 2-58.
FT REPEAT 2-59.
FT REPEAT 2-60.
FT REPEAT 2-61.
FT REPEAT 2-62.
FT REPEAT 2-63.
FT REPEAT 2-64.
FT REPEAT 2-65.
FT REPEAT 2-66.
FT REPEAT 2-67.
FT REPEAT 2-68.
FT REPEAT 2-69.
FT REPEAT 2-70.
FT REPEAT 2-71.
FT REPEAT 2-72.
FT REPEAT 2-73.
FT REPEAT 2-74.
FT REPEAT 2-75.
FT REPEAT 2-76.
FT REPEAT 2-77.
FT REPEAT 2-78.
FT REPEAT 2-79.
FT REPEAT 2-80.
FT REPEAT 2-81.
FT REPEAT 2-82.
FT REPEAT 2-83.
FT REPEAT 2-84.
FT REPEAT 2-85.
FT REPEAT 2-86.
FT REPEAT 2-87.
FT REPEAT 2-88.
FT REPEAT 2-89.
FT REPEAT 2-90.
FT REPEAT 2-91.
FT REPEAT 2-92.
FT REPEAT 2-93.
FT REPEAT 2-94.
FT REPEAT 2-95.
FT REPEAT 2-96.
FT REPEAT 2-97.
FT REPEAT 2-98.
FT REPEAT 2-99.
FT REPEAT 2-100.
FT REPEAT 2-101.
FT REPEAT 2-102.
FT REPEAT 2-103.
FT REPEAT 2-104.
FT REPEAT 2-105.
FT REPEAT 2-106.
FT REPEAT 2-107.
FT REPEAT 2-108.
FT REPEAT 2-109.
FT REPEAT 2-110.
FT REPEAT 2-111.
FT REPEAT 2-112.
FT REPEAT 2-113.
FT REPEAT 2-114.
FT REPEAT 2-115.
FT REPEAT 2-116.
FT REPEAT 2-117.
FT REPEAT 2-118.
FT REPEAT 2-119.
FT REPEAT 2-120.
FT REPEAT 2-121.
FT REPEAT 2-122.
FT REPEAT 2-123.
FT REPEAT 2-124.
FT REPEAT 2-125.
FT REPEAT 2-126.
FT REPEAT 2-127.
FT REPEAT 2-128.
FT REPEAT 2-129.
FT REPEAT 2-130.
FT REPEAT 2-131.
FT REPEAT 2-132.
FT REPEAT 2-133.
FT REPEAT 2-134.
FT REPEAT 2-135.
FT REPEAT 2-136.
FT REPEAT 2-137.
FT REPEAT 2-138.
FT REPEAT 2-139.
FT REPEAT 2-140.
FT REPEAT 2-141.
FT REPEAT 2-142.
FT REPEAT 2-143.
FT REPEAT 2-144.
FT REPEAT 2-145.
FT REPEAT 2-146.
FT REPEAT 2-147.
FT REPEAT 2-148.
FT REPEAT 2-149.
FT REPEAT 2-150.
FT REPEAT 2-151.
FT REPEAT 2-152.
FT REPEAT 2-153.
FT REPEAT 2-154.
FT REPEAT 2-155.
FT REPEAT 2-156.
FT REPEAT 2-157.
FT REPEAT 2-158.
FT REPEAT 2-159.
FT REPEAT 2-160.
FT REPEAT 2-161.
FT REPEAT 2-162.
FT REPEAT 2-163.
FT REPEAT 2-164.
FT REPEAT 2-165.
FT REPEAT 2-166.
FT REPEAT 2-167.
FT REPEAT 2-168.
FT REPEAT 2-169.
FT REPEAT 2-170.
FT REPEAT 2-171.
FT REPEAT 2-172.
FT REPEAT 2-173.
FT REPEAT 2-174.
FT REPEAT 2-175.
FT REPEAT 2-176.
FT REPEAT 2-177.
FT REPEAT 2-178.
FT REPEAT 2-179.
FT REPEAT 2-180.
FT REPEAT 2-181.
FT REPEAT 2-182.
FT REPEAT 2-183.
FT REPEAT 2-184.
FT REPEAT 2-185.
FT REPEAT 2-186.
FT REPEAT 2-187.
FT REPEAT 2-188.
FT REPEAT 2-189.
FT REPEAT 2-190.
FT REPEAT 2-191.
FT REPEAT 2-192.
FT REPEAT 2-193.
FT REPEAT 2-194.
FT REPEAT 2-195.
FT REPEAT 2-196.
FT REPEAT 2-197.
FT REPEAT 2-198.
FT REPEAT 2-199.
FT REPEAT 2-200.
FT REPEAT 2-201.
FT REPEAT 2-202.
FT REPEAT 2-203.
FT REPEAT 2-204.
FT REPEAT 2-205.
FT REPEAT 2-206.
FT REPEAT 2-207.
FT REPEAT 2-208.
FT REPEAT 2-209.
FT REPEAT 2-210.
FT REPEAT 2-211.
FT REPEAT 2-212.
FT REPEAT 2-213.
FT REPEAT 2-214.
FT REPEAT 2-215.
FT REPEAT 2-216.
FT REPEAT 2-217.
FT REPEAT 2-218.
FT REPEAT 2-219.
FT REPEAT 2-220.
FT REPEAT 2-221.
FT REPEAT 2-222.
FT REPEAT 2-223.
FT REPEAT 2-224.
FT REPEAT 2-225.
FT REPEAT 2-226.
FT REPEAT 2-227.
FT REPEAT 2-228.
FT REPEAT 2-229.
FT REPEAT 2-230.
FT REPEAT 2-231.
FT REPEAT 2-232.
FT REPEAT 2-233.
FT REPEAT 2-234.
FT REPEAT 2-235.
FT REPEAT 2-236.
FT REPEAT 2-237.
FT REPEAT 2-238.
FT REPEAT 2-239.
FT REPEAT 2-240.
FT REPEAT 2-241.
FT REPEAT 2-242.
FT REPEAT 2-243.
FT REPEAT 2-244.
FT REPEAT 2-245.
FT REPEAT 2-246.
FT REPEAT 2-247.
FT REPEAT 2-248.
FT REPEAT 2-249.
FT REPEAT 2-250.
FT REPEAT 2-251.
FT REPEAT 2-252.
FT REPEAT 2-253.
FT REPEAT 2-254.
FT REPEAT 2-255.
FT REPEAT 2-256.
FT REPEAT 2-257.
FT REPEAT 2-258.
FT REPEAT 2-259.
FT REPEAT 2-260.
FT REPEAT 2-261.
FT REPEAT 2-262.
FT REPEAT 2-263.
FT REPEAT 2-264.
FT REPEAT 2-265.
FT REPEAT 2-266.
FT REPEAT 2-267.
FT REPEAT 2-268.
FT REPEAT 2-269.
FT REPEAT 2-270.
FT REPEAT 2-271.
FT REPEAT 2-272.
FT REPEAT 2-273.
FT REPEAT 2-274.
FT REPEAT 2-275.
FT REPEAT 2-276.
FT REPEAT 2-277.
FT REPEAT 2-278.
FT REPEAT 2-279.
FT REPEAT 2-280.
FT REPEAT 2-281.
FT REPEAT 2-282.
FT REPEAT 2-283.
FT REPEAT 2-284.
FT REPEAT 2-285.
FT REPEAT 2-286.
FT REPEAT 2-287.
FT REPEAT 2-288.
FT REPEAT 2-289.
FT REPEAT 2-290.
FT REPEAT 2-291.
FT REPEAT 2-292.
FT REPEAT 2-293.
FT REPEAT 2-294.
FT REPEAT 2-295.
FT REPEAT 2-296.
FT REPEAT 2-297.
FT REPEAT 2-298.
FT REPEAT 2-299.
FT REPEAT 2-300.
FT REPEAT 2-301.
FT REPEAT 2-302.
FT REPEAT 2-303.
FT REPEAT 2-304.
FT REPEAT 2-305.
FT REPEAT 2-306.
FT REPEAT 2-307.
FT REPEAT 2-308.
FT REPEAT 2-309.
FT REPEAT 2-310.
FT REPEAT 2-311.
FT REPEAT 2-312.
FT REPEAT 2-313.
FT REPEAT 2-314.
FT REPEAT 2-315.
FT REPEAT 2-316.
FT REPEAT 2-317.
FT REPEAT 2-318.
FT REPEAT 2-319.
FT REPEAT 2-320.
FT REPEAT 2-321.
FT REPEAT 2-322.
FT REPEAT 2-323.
FT REPEAT 2-324.
FT REPEAT 2-325.
FT REPEAT 2-326.
FT REPEAT 2-327.
FT REPEAT 2-328.
FT REPEAT 2-329.
FT REPEAT 2-330.
FT REPEAT 2-331.
FT REPEAT 2-332.
FT REPEAT 2-333.
FT REPEAT 2-334.
FT REPEAT 2-335.
FT REPEAT 2-336.
FT REPEAT 2-337.
FT REPEAT 2-338.
FT REPEAT 2-339.
FT REPEAT 2-340.
FT REPEAT 2-341.
FT REPEAT 2-342.
FT REPEAT 2-343.
FT REPEAT 2-344.
FT REPEAT 2-345.
FT REPEAT 2-346.
FT REPEAT 2-347.
FT REPEAT 2-348.
FT REPEAT 2-349.
FT REPEAT 2-350.
FT REPEAT 2-351.
FT REPEAT 2-352.
FT REPEAT 2-353.
FT REPEAT 2-354.
FT REPEAT 2-355.
FT REPEAT 2-356.
FT REPEAT 2-357.
FT REPEAT 2-358.
FT REPEAT 2-359.
FT REPEAT 2-360.
FT REPEAT 2-361.
FT REPEAT 2-362.
FT REPEAT 2-363.
FT REPEAT 2-364.
FT REPEAT 2-365.
FT REPEAT 2-366.
FT REPEAT 2-367.
FT REPEAT 2-368.
FT REPEAT 2-369.
FT REPEAT 2-370.
FT REPEAT 2-371.
FT REPEAT 2-372.
FT REPEAT 2-373.
FT REPEAT 2-374.
FT REPEAT 2-375.
FT REPEAT 2-376.
FT REPEAT 2-377.
FT REPEAT 2-378.
FT REPEAT 2-379.
FT REPEAT 2-380.
FT REPEAT 2-381.
FT REPEAT 2-382.
FT REPEAT 2-383.
FT REPEAT 2-384.
FT REPEAT 2-385.
FT REPEAT 2-386.
FT REPEAT 2-387.
FT REPEAT 2-388.
FT REPEAT 2-389.
FT REPEAT 2-390.
FT REPEAT 2-391.
FT REPEAT 2-392.
FT REPEAT 2-393.
FT REPEAT 2-394.
FT REPEAT 2-395.
FT REPEAT 2-396.
FT REPEAT 2-397.
FT REPEAT 2-398.
FT REPEAT 2-399.
FT REPEAT 2-400.
FT REPEAT 2-401.
FT REPEAT 2-402.
FT REPEAT 2-403.
FT REPEAT 2-404.
FT REPEAT 2-405.
FT REPEAT 2-406.
FT REPEAT 2-407.
FT REPEAT 2-408.
FT REPEAT 2-409.
FT REPEAT 2-410.
FT REPEAT 2-411.
FT REPEAT 2-412.
FT REPEAT 2-413.
FT REPEAT 2-414.
FT REPEAT 2-415.
FT REPEAT 2-416.
FT REPEAT 2-417.
FT REPEAT 2-418.
FT REPEAT 2-419.
FT REPEAT 2-420.
FT REPEAT 2-421.
FT REPEAT 2-422.
FT REPEAT 2-423.
FT REPEAT 2-424.
FT REPEAT 2-425.
FT REPEAT 2-426.
FT REPEAT 2-427.
FT REPEAT 2-428.
FT REPEAT 2-429.
FT REPEAT 2-430.
FT REPEAT 2-431.
FT REPEAT 2-432.
FT REPEAT 2-433.
FT REPEAT 2-434.
FT REPEAT 2-435.
FT REPEAT 2-436.
FT REPEAT 2-437.
FT REPEAT 2-438.
FT REPEAT 2-439.
FT REPEAT 2-440.
FT REPEAT 2-441.
FT REPEAT 2-442.
FT REPEAT 2-443.
FT REPEAT 2-444.
FT REPEAT 2-445.
FT REPEAT 2-446.
FT REPEAT 2-447.
FT REPEAT 2-448.
FT REPEAT 2-449.
FT REPEAT 2-450.
FT REPEAT 2-451.
FT REPEAT 2-452.
FT REPEAT 2-453.
FT REPEAT 2-454.
FT REPEAT 2-455.
FT REPEAT 2-456.
FT REPEAT 2-457.
FT REPEAT 2-458.
FT REPEAT 2-459.
FT REPEAT 2-460.
FT REPEAT 2-461.
FT REPEAT 2-462.
FT REPEAT 2-463.
FT REPEAT 2-464.
FT REPEAT 2-465.
FT REPEAT 2-466.
FT REPEAT 2-467.
FT REPEAT 2-468.
FT REPEAT 2-469.
FT REPEAT 2-470.
FT REPEAT 2-471.
FT REPEAT 2-472.
FT REPEAT 2-473.
FT REPEAT 2-474.
FT REPEAT 2-475.
FT REPEAT 2-476.
FT REPEAT 2-477.
FT REPEAT 2-478.
FT REPEAT 2-479.
FT REPEAT 2-480.
FT REPEAT 2-481.
FT REPEAT 2-482.
FT REPEAT 2-483.
FT REPEAT 2-484.
FT REPEAT 2-485.
FT REPEAT 2-486.
FT REPEAT 2-487.
FT REPEAT 2-488.
FT REPEAT 2-489.
FT REPEAT 2-490.
FT REPEAT 2-491.
FT REPEAT 2-492.
FT REPEAT 2-493.
FT REPEAT 2-494.
FT REPEAT 2-495.
FT REPEAT 2-496.
FT REPEAT 2-497.
FT REPEAT 2-498.
FT REPEAT 2-499.
FT REPEAT 2-500.
FT REPEAT 2-501.
FT REPEAT 2-502.
FT REPEAT 2-503.
FT REPEAT 2-504.
FT REPEAT 2-505.
FT REPEAT 2-506.
FT REPEAT 2-507.
FT REPEAT 2-508.
FT REPEAT 2-509.
FT REPEAT 2-510.
FT REPEAT 2-511.
FT REPEAT 2-512.
FT REPEAT 2-513.
FT REPEAT 2-514.
FT REPEAT 2-515.
FT REPEAT 2-516.
FT REPEAT 2-517.
FT REPEAT 2-518.
FT REPEAT 2-519.
FT REPEAT 2-520.
FT REPEAT 2-521.
FT REPEAT 2-522.
FT REPEAT 2-523.
FT REPEAT 2-524.
FT REPEAT 2-525.
FT REPEAT 2-526.
FT REPEAT 2-527.
FT REPEAT 2-528.
FT REPEAT 2-529.
FT REPEAT 2-530.
FT REPEAT 2-531.
FT REPEAT 2-532.
FT REPEAT 2-533.
FT REPEAT 2-534.
FT REPEAT 2-535.
FT REPEAT 2-536.
FT REPEAT 2-537.
FT REPEAT 2-538.
FT REPEAT 2-539.
FT REPEAT 2-540.
FT REPEAT 2-541.
FT REPEAT 2-542.
FT REPEAT 2-543.
FT REPEAT 2-544.
FT REPEAT 2-545.
FT REPEAT 2-546.
FT REPEAT 2-547.
FT REPEAT 2-548.
FT REPEAT 2-549.
FT REPEAT 2-550.
FT REPEAT 2-551.
FT REPEAT 2-552.
FT REPEAT 2-553.
FT REPEAT 2-554.
FT REPEAT 2-555.
FT REPEAT 2-556.
FT REPEAT 2-557.
FT REPEAT 2-558.
FT REPEAT 2-559.
FT REPEAT 2-560.
FT REPEAT 2-561.
FT REPEAT 2-562.
FT REPEAT 2-563.
FT REPEAT 2-564.
FT REPEAT 2-565.
FT REPEAT 2-566.
FT REPEAT 2-567.
FT REPEAT 2-568.
FT REPEAT 2-569.
FT REPEAT 2-570.
FT REPEAT 2-571.
FT REPEAT 2-572.
FT REPEAT 2-573.
FT REPEAT 2-574.
FT REPEAT 2-575.
FT REPEAT 2-576.
FT REPEAT 2-577.
FT REPEAT 2-578.
FT REPEAT 2-579.
FT REPEAT 2-580.
FT REPEAT 2-581.
FT REPEAT 2-582.
FT REPEAT 2-583.
FT REPEAT 2-584.
FT REPEAT 2-585.
FT REPEAT 2-586.
FT REPEAT 2-587.
FT REPEAT 2-588.
FT REPEAT 2-589.
FT REPEAT 2-590.
FT REPEAT 2-591.
FT REPEAT 2-592.
FT REPEAT 2-593.
FT REPEAT 2-594.
FT REPEAT 2-595.
FT REPEAT 2-596.
FT REPEAT 2-597.
FT REPEAT 2-598.
FT REPEAT 2-599.
FT REPEAT 2-600.
FT REPEAT 2-601.
FT REPEAT 2-602.
FT REPEAT 2-603.
FT REPEAT 2-604.
FT REPEAT 2-605.
FT REPEAT 2-606.
FT REPEAT 2-607.
FT REPEAT 2-608.
FT REPEAT 2-609.
FT REPEAT 2-610.
FT REPEAT 2-611.
FT REPEAT 2-612.
FT REPEAT 2-613.
FT REPEAT 2-614.
FT REPEAT 2-615.
FT REPEAT 2-616.
FT REPEAT 2-617.
FT REPEAT 2-618.
FT REPEAT 2-619.
FT REPEAT 2-620.
FT REPEAT 2-621.
FT REPEAT 2-622.
FT REPEAT 2-623.
FT REPEAT 2-624.
FT REPEAT 2-625.
FT REPEAT 2-626.
FT REPEAT 2-627.
FT REPEAT 2-628.
FT REPEAT 2-629.
FT REPEAT 2-630.
FT REPEAT 2-631.
FT REPEAT 2-632.
FT REPEAT 2-633.
FT REPEAT 2-634.
FT REPEAT 2-635.
FT REPEAT 2-636.
FT REPEAT 2-637.
FT REPEAT 2-638.
FT REPEAT 2-639.
FT REPEAT 2-640.
FT REPEAT 2-641.
FT REPEAT 2-642.
FT REPEAT 2-643.
FT REPEAT 2-644.
FT REPEAT 2-645.
FT REPEAT 2-646.
FT REPEAT 2-647.
FT REPEAT 2-648.
FT REPEAT 2-649.
FT REPEAT 2-650.
FT REPEAT 2-651.
FT REPEAT 2-652.
FT REPEAT 2-653.
FT REPEAT 2-654.
FT REPEAT 2-655.
FT REPEAT 2-656.
FT REPEAT 2-657.
FT REPEAT 2-658.
FT REPEAT 2-659.
FT REPEAT 2-660.
FT REPEAT 2-661.
FT REPEAT 2-662.
FT REPEAT 2-663.
FT REPEAT 2-664.
FT REPEAT 2-665.
FT REPEAT 2-666.
FT REPEAT 2-667.
FT REPEAT 2-668.
FT REPEAT 2-669.
FT REPEAT 2-670.
FT REPEAT 2-671.
FT REPEAT 2-672.
FT REPEAT 2-673.
FT REPEAT 2-674.
FT REPEAT 2-675.
FT REPEAT 2-676.
FT REPEAT 2-677.
FT REPEAT 2-678.
FT REPEAT 2-679.
FT REPEAT 2-680.
FT REPEAT 2-681.
FT REPEAT 2-682.
FT REPEAT 2-683.
FT REPEAT 2-684.
FT REPEAT 2-685.
FT REPEAT 2-686.
FT REPEAT 2-687.
FT REPEAT 2-688.
FT REPEAT 2-689.
FT REPEAT 2-690.
FT REPEAT 2-691.
FT REPEAT 2-692.
FT REPEAT 2-693.
FT REPEAT 2-694.
FT REPEAT 2-695.
FT REPEAT 2-696.
FT REPEAT 2-697.
FT REPEAT 2-698.
FT REPEAT 2-699.
FT REPEAT 2-700.
FT REPEAT 2-701.
FT REPEAT 2-702.
FT REPEAT 2-703.
FT REPEAT 2-704.
FT REPEAT 2-705.
FT REPEAT 2-706.
FT REPEAT 2-707.
FT REPEAT 2-708.
FT REPEAT 2-709.
FT REPEAT 2-710.
FT REPEAT 2-711.
FT REPEAT 2-712.
FT REPEAT 2-713.
FT REPEAT 2-714.
FT REPEAT 2-715.
FT REPEAT 2-716.
FT REPEAT 2-717.
FT REPEAT 2-718.
FT REPEAT 2-719.
FT REPEAT 2-720.
FT REPEAT 2-721.
FT REPEAT 2-722.
FT REPEAT 2-723.
FT REPEAT 2-724.
FT REPEAT 2-725.
FT REPEAT 2-726.
FT REPEAT 2-727.
FT REPEAT 2-728.
FT REPEAT 2-729.
FT REPEAT 2-730.
FT REPEAT 2-731.
FT REPEAT 2-732.
FT REPEAT 2-733.
FT REPEAT 2-734.
FT REPEAT 2-735.
FT REPEAT 2-736.
FT REPEAT 2-737.
FT REPEAT 2-738.
FT REPEAT 2-739.
FT REPEAT 2-740.
FT REPEAT 2-741.
FT REPEAT 2-742.
FT REPEAT 2-743.
FT REPEAT 2-744.
FT REPEAT 2-745.
FT REPEAT 2-746.
FT REPEAT 2-747.
FT REPEAT 2-748.
FT REPEAT 2-749.
FT REPEAT 2-750.
FT REPEAT 2-751.
FT REPEAT 2-752.
FT REPEAT 2-753.
FT REPEAT 2-754.
FT REPEAT 2-755.
FT REPEAT 2-756.
FT REPEAT 2-757.
FT REPEAT 2-758.
FT REPEAT 2-759.
FT REPEAT 2-760.
FT REPEAT 2-761.
FT REPEAT 2-762.
FT REPEAT 2-763.
FT REPEAT 2-764.
FT REPEAT 2-765.
FT REPEAT 2-766.
FT REPEAT 2-767.
FT REPEAT 2-768.
FT REPEAT 2-769.
FT REPEAT 2-770.
FT REPEAT 2-771.
FT REPEAT 2-772.
FT REPEAT 2-773.
FT REPEAT 2-774.
FT REPEAT 2-775.
FT REPEAT 2-776.
FT REPEAT 2-777.
FT REPEAT 2-778.
FT REPEAT 2-779.
FT REPEAT 2-780.
FT REPEAT 2-781.
FT REPEAT 2-782.
FT REPEAT 2-783.
FT REPEAT 2-784.
FT REPEAT 2-785.
FT REPEAT 2-786.
FT REPEAT 2-787.
FT REPEAT 2-788.
FT REPEAT 2-789.
FT REPEAT 2-790.
FT REPEAT 2-791.
FT REPEAT 2-792.
FT REPEAT 2-793.
FT REPEAT 2-794.
FT REPEAT 2-795.
FT REPEAT 2-796.
FT REPEAT 2-797.
FT REPEAT 2-798.
FT REPEAT 2-799.
FT REPEAT 2-800.
FT REPEAT 2-801.
FT REPEAT 2-802.
FT REPEAT 2-803.
FT REPEAT 2-804.
FT REPEAT 2-805.
FT REPEAT 2-806.
FT REPEAT 2-807.
FT REPEAT 2-808.
FT REPEAT 2-809.
FT REPEAT 2-810.
FT REPEAT 2-811.
FT REPEAT 2-812.
FT REPEAT 2-813.
FT REPEAT 2-814.
FT REPEAT 2-815.
FT REPEAT 2-816.
FT REPEAT 2-817.
FT REPEAT 2-818.
FT REPEAT 2-819.
FT REPEAT 2-820.
FT REPEAT 2-821.
FT REPEAT 2-822.
FT REPEAT 2-823.
FT REPEAT 2-824.
FT REPEAT 2-825.
FT REPEAT 2-826.
FT REPEAT 2-827.
FT REPEAT 2-828.
FT REPEAT 2-829.
FT REPEAT 2-830.
FT REPEAT 2-831.
FT REPEAT 2-832.
FT REPEAT 2-833.
FT REPEAT 2-834.
FT REPEAT 2-835.
FT REPEAT 2-836.
FT REPEAT 2-837.
FT REPEAT 2-838.
FT REPEAT 2-839.
FT REPEAT 2-840.
FT REPEAT 2-841.
FT REPEAT 2-842.
FT REPEAT 2-843.
FT REPEAT 2-844.
FT REPEAT 2-845.
FT REPEAT 2-846.
FT REPEAT 2-847.
FT REPEAT 2-848.
FT REPEAT 2-849.
FT REPEAT 2-850.
FT REPEAT 2-851.
FT REPEAT 2-852.
FT REPEAT 2-853.
FT REPEAT 2-854.
FT REPEAT 2-855.
FT REPEAT 2-856.
FT REPEAT 2-857.
FT REPEAT 2-858.
FT REPEAT 2-859.
FT REPEAT 2-860.
FT REPEAT 2-861.
FT REPEAT 2-862.
FT REPEAT 2-863.
FT REPEAT 2-864.
FT REPEAT 2-865.
FT REPEAT 2-866.
FT REPEAT 2-867.
FT REPEAT 2-868.
FT REPEAT 2-869.
```


MEDLINE=20052169; PubMed=10586886;
 RA Macedo-Ribeiro S., Bode W., Huber R., Quinn-Allen M.A., Kim S.W.,
 RA Ortel T.L., Bourenkov G.P., Bartunik H.D., Stubbs M.T., Kane W.H.,
 RA Fuentes-Prior P.;
 RT "Crystal structures of the membrane-binding C2 domain of human
 RT coagulation factor V";
 RL Nature 402:434-439(1999).
 [9]
 RP VARIANT MET-1764.
 RX MEDLINE=95179146; PubMed=7874144;
 RA Bayston T.A., Ireland H., Olds R.J., Thein S.L., Lane D.A.;
 RT "A polymorphism in the human coagulation factor V gene";
 RL Hum. Mol. Genet. 3:2085-2085(1994).
 [10]
 RP VARIANT APCR GLN-534.
 RX MEDLINE=94217810; PubMed=8164741;
 RA Bertina R.M., Koelenan B.P.C., Koster T., Rosendaal P.R.,
 RA Dirven R.J., de Ronde H., van der Velden P.A., Reitsma P.H.;
 RT "Mutation in blood coagulation factor V associated with resistance to
 RT activated protein C";
 RL Nature 369:64-67(1994).
 [11]
 RP VARIANTS ILE-1285 AND ARG-1327.
 RX MEDLINE=96351768; PubMed=9713778;
 RA Lunghi B., Iacoviello L., Gemmati D., Dilasio M.G., Castoldi E.,
 RA Pinotti M., Castaman G., Redaelli R., Mariani G., Marchetti G.,
 RA Bernardi F.;
 RT "Detection of new polymorphic markers in the factor V gene:
 RT association with factor V levels in plasma";
 RL Thromb. Haemost. 75:45-48(1996).
 [12]
 RP VARIANT APCR GLY-334, AND VARIANT LYS-513.
 RX MEDLINE=98122763; PubMed=9454741;
 RA Chan W.P., Lee C.K., Kwong Y.L., Lam C.K., Liang R.;
 RT "A novel mutation of Arg306 of factor V gene in Hong Kong Chinese";
 RL Blood 91:1135-1139(1998).
 [13]
 RP VARIANT APCR THR-334.
 RX MEDLINE=98122764; PubMed=9454742;
 RA Williamson D., Brown K., Luddington R., Baglin C., Baglin T.;
 RT "Factor V Cambridge: a new mutation (Arg306-to-Thr) associated with
 RT resistance to activated protein C";
 RL Blood 91:1140-1144(1998).
 [14]
 RP VARIANTS HIS-107; THR-413; LYS-513; SER-809; THR-817; ARG-858;
 RP ARG-865; GLU-925; GLN-1146; ALA-1530; SER-1685; VAL-1749; MET-1764;
 RP ILS-1820 AND GLY-2222, AND VARIANT APCR GLN-534.
 RX MEDLINE=99318093; PubMed=10391209;
 RA Cargill M., Altschuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
 RA Shaw N., Lane C.R., Lim E.P., Kalyanaram N., Nemes J., Ziaugra L.,
 RA Friedland L., Rolfe A., Warrington J., Lipschutz R., Daley G.Q.,
 RA Lander E.S.;
 RT "Characterization of single-nucleotide polymorphisms in coding regions
 RT of human genes";
 RL Nat. Genet. 22:231-238(1999).
 [15]
 RP ERRATUM.
 RA Cargill M., Altschuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
 RA Shaw N., Lane C.R., Lim E.P., Kalyanaram N., Nemes J., Ziaugra L.,
 RA Friedland L., Rolfe A., Warrington J., Lipschutz R., Daley G.Q.,
 RA Lander E.S.;
 RL Nat. Genet. 23:373-373(1999).
 [16]
 RP VARIANT APCR HIS-2102.
 RX MEDLINE=21847288; PubMed=11858490;
 RA Schrijver I., Houissa-Kastally R., Jones C.D., Garcia K.C.,
 RA Zehnder J.L.;
 RT "Novel factor V C2-domain mutation (R2074H) in two families with
 RT factor V deficiency and bleeding";
 RL Thromb. Haemost. 87:294-299(2002).
 CC -1- FUNCTION: Coagulation factor V is a cofactor that participates
 CC with factor Xa to activate prothrombin to thrombin.
 CC -1- SUBUNIT: Factor Va is composed of a heavy chain and a light

chain, noncovalently bound. The interaction between the two chains
 is calcium-dependent.
 CC -1- DOMAIN: Domain B contains 35 x 9 AA tandem repeats, and 2 x 17 AA
 CC repeats.
 CC -1- PTM: Thrombin activates factor V proteolytically to the active
 CC cofactor, factor Va (formation of a heavy chain at the N-
 CC terminus and a light chain at the C-terminus).
 CC -1- PTM: Sulfation is required for efficient thrombin cleavage and
 CC activation and for full procoagulant activity.
 CC -1- DISEASE: Defects in F5 are the cause of Owren parahemophilia
 CC [MIM:227400], an hemorrhagic diastasis.
 CC -1- DISEASE: Defects in F5 are the cause of resistance to activated
 CC protein C (APCR) [MIM:188055], a form of thrombophilia. The APCR
 CC mutation is found in about 5% of the population which suggest that
 CC a slight thrombotic tendency may confer some advantage in fetal
 CC implantation.
 CC -1- SIMILARITY: Contains 3 F5/8 type A domains.
 CC -1- SIMILARITY: Contains 2 F5/8 type C domains.
 CC -1- SIMILARITY: STRONG, TO COAGULATION FACTOR VIII.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; L32779; AAB59401.1; JOINED.
 CC EMBL; L32755; AAB59401.1; JOINED.
 CC EMBL; L32756; AAB59401.1; JOINED.
 CC EMBL; L32757; AAB59401.1; JOINED.
 CC EMBL; L32758; AAB59401.1; JOINED.
 CC EMBL; L32759; AAB59401.1; JOINED.
 CC EMBL; L32760; AAB59401.1; JOINED.
 CC EMBL; L32761; AAB59401.1; JOINED.
 CC EMBL; L32762; AAB59401.1; JOINED.
 CC EMBL; L32763; AAB59401.1; JOINED.
 CC EMBL; L32764; AAB59401.1; JOINED.
 CC EMBL; L32765; AAB59401.1; JOINED.
 CC EMBL; L32766; AAB59401.1; JOINED.
 CC EMBL; L32767; AAB59401.1; JOINED.
 CC EMBL; L32768; AAB59401.1; JOINED.
 CC EMBL; L32769; AAB59401.1; JOINED.
 CC EMBL; L32770; AAB59401.1; JOINED.
 CC EMBL; L32771; AAB59401.1; JOINED.
 CC EMBL; L32772; AAB59401.1; JOINED.
 CC EMBL; L32773; AAB59401.1; JOINED.
 CC EMBL; L32774; AAB59401.1; JOINED.
 CC EMBL; L32775; AAB59401.1; JOINED.
 CC EMBL; L32776; AAB59401.1; JOINED.
 CC EMBL; L32777; AAB59401.1; JOINED.
 CC EMBL; L32778; AAB59401.1; JOINED.
 CC EMBL; M16967; AAB52424.1; -.
 CC EMBL; M14335; AAB59532.1; -.
 CC PDB; 1CZS; 26-NOV-99.
 CC PDB; 1CZT; 28-NOV-99.
 CC PDB; 1CZV; 28-NOV-99.
 CC PDB; 1FV4; 17-JAN-01.
 CC Genew; HGNC:3542; F5.
 CC MIM; 227400; -.
 CC MIM; 134400; -.
 CC MIM; 188055; -.
 Query March 43.2%; Score 376; DB 1; Length 2224;
 Best Local Similarity 41.9%; Pred. No. 3.7e-28;
 Matches 70; Conservative 38; Mismatches 53; Indels 6; Gaps 3;
 QY 1 CDLNSCSMPLGMSKATSDAQITASSVFTNMAT-WSPSKARLHLOGRANAEPOVNNPK 59
 Db 2061 CEVNGCSTPLGMEKNGKIKQITASSFKSWGDYEPFRARLNAQGRVNAQAKANNK 2120
 QY 60 EWLQVDFQKTMKVTGVTTCQVKSLTSMYVKEFLISSQDGHQWTLFFQNGKV--KVFQ 117

FT	DISULFID	73	96	BY SIMILARITY.
FT	DISULFID	98	107	BY SIMILARITY.
FT	DISULFID	111	267	BY SIMILARITY.
FT	DISULFID	254	258	BY SIMILARITY.
FT	DISULFID	272	427	BY SIMILARITY.
FT	SITE	87	89	CELL ATTACHMENT SITE (POTENTIAL).
FT	CARBOHYD	61	61	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	230	230	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	280	280	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	390	390	N-LINKED (GLCNAC. .) (POTENTIAL).
SQ	SEQUENCE	427 AA;	47413 MW;	E8C8631F3EE6047 CRC64;

Query Match 42.2%; Score 367.5; DB 1; Length 427;
Best Local Similarity 45.3%; Pred. No. 3.5e-28;
Matches 73; Conservative 28; Mismatches 57; Indels 3; Gaps 2;

QY	1	CDLNSGMPGLGMSKAISDAQITASSYFT--NWFA-TWSPSKARLHLOGRBNARPOVNN	57
Db	267	CELHGCSEPLGLKNITPDSQITASSYKTNWLRFAFGWYPHLGRDNGQKINAWTAOSNS	326
QY	58	PKRWLOVDFTKMKVGTGVTQGVKSLTSMYVKEFTISSQDGHQWTLFFQNGKVKVFG	117
Db	327	AKEWLOVDLGTQKVKYGIITQGFARDPFGHIOVASYKVVAHSDGQVWTVVEEQGTSKVFG	386
QY	118	NQDSFTFVNSLDPPLTRYLRTHPQSWHQIALRMEVLGC	158
Db	387	NLDNNSHKKIPEKPFEMARYVRVPLPSWNRITIRLELGC	427

RESULT 8
MFGM MOUSE STANDARD; PRT; 463 AA.
ID MFGM MOUSE
AC P21956; P97800;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Lactadherin precursor (Milk fat globule-EGF factor 8) (MFGM) (MFGM)
DE (Sperm surface protein SP47) (MP47).
OS MFGES8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A., AND SEQUENCE OF 23-35.
RP TISSUE=Mammary gland;
RC TISSUE=Mammary gland;
RX MEDLINE=9104608; PubMed=2122462;
RA Stubbs J.D., Lekutis C., Singer K.L., Bui A., Yuzuki D.,
RA Srinivasan U., Parry G.;
RT "cDNA cloning of a mouse mammary epithelial cell surface protein
RT reveals the existence of epidermal growth factor-like domains linked
RT to factor VIII-like sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 87:8417-8421 (1990).
[2]
RP SEQUENCE OF 23-463 FROM N.A.
RC TISSUE=Testis;
RA Enselin M.A.;
RL Submitted (NOV-1997) to the ENBL/GenBank/DBJ databases.
CC -!- FUNCTION: May be involved in phospholipid binding. Zona pellucida-
CC binding protein.
CC -!- SUBCELLULAR LOCATION: Peripheral membrane protein.
CC -!- TISSUE SPECIFICITY: Mammary epithelial cell surfaces and
CC spermatozoan.
CC -!- DEVELOPMENTAL STAGE: mRNA expression is detectable in mammary
CC tissue from nonpregnant animals and maximal in the lactating
CC gland.
CC -!- SIMILARITY: Contains 2 EGF-like domains.
CC -!- SIMILARITY: Contains 2 PF/8 type C domains.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way

modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

EMBL; M38337; AAA39534.1; -
 EMBL; Y11684; CAA72380.1; -
 PIR; A36479; A36479.
 HSSP; P00740; IEDM.
 MGI; MGI:102768; Mfge8.
 InterPro; IPR001438; EGF II.
 InterPro; IPR006209; EGF-like.
 InterPro; IPR000421; FA58_C.
 InterPro; IPR008979; Gal_Bind_like.
 InterPro; IPR006210; IEGF.
 Pfam; PF00008; EGF; 2.
 Pfam; PF00754; F5_F8 type C; 2.
 PRINTS; PR00010; EGFLOOD.
 SMART; SM00181; EGF; 2.
 SMART; SM00231; FA58C; 2.
 PROSITE; PS00022; EGF_1; 2.
 PROSITE; PS01186; EGF_2; 2.
 PROSITE; PS00026; EGF_3; 2.
 PROSITE; PS01285; FA58C_1; 2.
 PROSITE; PS01285; FA58C_2; 2.
 PROSITE; PS00022; FA58C_3; 2.
 Signal; Glycoprotein; Repeat; EGF-like domain; Milk.
 SIGNAL 1 22
 CHAIN 23 463
 DOMAIN 24 61
 DOMAIN 64 108
 DOMAIN 148 303
 DOMAIN 308 463
 SITE 87 89
 DISULFID 28 39
 DISULFID 33 49
 BY SIMILARITY.
 BY SIMILARITY.
 BY SIMILARITY.
 BY SIMILARITY.
 BY SIMILARITY.
 BY SIMILARITY.
 BY SIMILARITY.
 BY SIMILARITY.
 BY SIMILARITY.
 BY SIMILARITY.
 BY SIMILARITY.
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 S -> F (IN REF. 2).
 N -> D (IN REF. 1; AA SEQUENCE).
 ETNYNLDGEYMETTAVPTAVPTAPTDLNLSLR ->
 G (IN REF. 2).
 Y -> S (IN REF. 2).
 H -> T (IN REF. 2).
 L -> S (IN REF. 2).
 E -> A (IN REF. 2).
 Query Match 40.6%; Score 353.5; DB 1; Length 463;
 Best Local Similarity 42.9%; Pred. No. 8.7e-27;
 Matches 69; Conservative 32; Mismatches 57; Indels 3; Gaps 2;
 QY 1 CDLNSGMPGLGMSKAISSAQITASSYFT--NNFA-TWSPSKARLHLQGRSNAMKPVQNN 57
 Db 303 CELHGLEFLGLKNTIPDSOMSSASYKTNLRAFPGWYPHLGRLDNCKINAWTAQNS 362
 QY 58 PKEWLQVDFOKTKVGTGVTQGVKSLTSMYKVEFLISSQDGHQWTLFFQNGKVKVFG 117
 Db 363 AKENLQVDLGTQVGTGTLTGARDFGHGYVESYKVAHSDGVQWTVIEGSSKVFQ 422
 QY 118 NQDSFTPVNSLDPPLLTRYLRHPSQVWHQIALRMEVLGC 158
 Db 423 NLDNNSHKKNIFKPPMRYVRYVLPVSWHNRITLRLGLGC 463

RESULT 9
 NRP2 RAT
 ID NRP2 RAT STANDARD; PRT; 925 AA.
 AC O35276;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Neuropilin-2 precursor (Vascular endothelial cell growth factor 165
 DE receptor 2).
 GN NRP2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1] _TaxID=10116;
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=97433085; PubMed=9288754;
 RA Kolodkin A.L., Levengood D.V., Rowe E.G., Tai Y.-T., Giger R.J.,
 RA Ginty D.D.;
 RT "Neuropilin is a semaphorin III receptor.";
 RL Cell 90:753-762(1997);
 CC -!- FUNCTION: High affinity receptor for semaphorins 3C, 3P, VEGF-165
 CC and VEGF-145 isoforms of VEGF, and the PLGF-2 isoform of PGF.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: Found in certain neuronal populations of the
 CC CNS and in other nonneuronal tissues including mesenchymal tissue
 CC lining in the ribs.
 CC -!- SIMILARITY: Belongs to the neuropilin family.
 CC -!- SIMILARITY: Contains 2 CUB domains.
 CC -!- SIMILARITY: Contains 2 F5/8 type C domains.
 CC -!- SIMILARITY: Contains 1 MAM domain.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

EMBL; AF016297; AAC53338.1; -
 HSSP; P12259; 1CZT
 InterPro; IPR000859; CUB.
 InterPro; IPR000421; FA58_C.
 InterPro; IPR008979; Gal_Bind like.
 InterPro; IPR000998; MAM_domain.
 Pfam; PF00431; CUB; 2.
 Pfam; PF00754; F5_F8 type C; 2.
 Pfam; PF00629; MAM; 1.
 PRINTS; PR00020; MAMDOMAIN.
 SMART; SM00042; CUB; 2.
 SMART; SM00231; FA58C; 2.
 SMART; SM00137; MAM; 1.
 PROSITE; PS01180; CUB; 2.
 PROSITE; PS01285; FA58C_1; 2.
 PROSITE; PS01285; FA58C_2; 2.
 PROSITE; PS00022; FA58C_3; 2.
 PROSITE; PS00060; MAM; 2; 1.
 Transmembrane; Glycoprotein;
 SIGNAL 1 22
 CHAIN 23 925
 DOMAIN 23 858
 TRANSMEM 859 883
 DOMAIN 884 925
 DOMAIN 28 142
 DOMAIN 149 267
 DOMAIN 277 427
 DOMAIN 434 592
 DOMAIN 642 802
 DISULFID 28 55
 DISULFID 83 105
 DISULFID 149 175
 Neurone; Signal; Repeat; Receptor.
 POTENTIAL.
 NEUROPILIN-2.
 EXTRACELLULAR (POTENTIAL).
 POTENTIAL.
 CYTOPLASMIC (POTENTIAL).
 CUB 1.
 CUB 2.
 F5/8 TYPE C 1.
 F5/8 TYPE C 2.
 MAM.
 BY SIMILARITY.
 BY SIMILARITY.
 BY SIMILARITY.

```
FT DISULFID 208 230 BY SIMILARITY.
FT DISULFID 277 427 BY SIMILARITY.
FT DISULFID 434 592 BY SIMILARITY.
FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 629 629 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 833 833 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 834 834 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 925 AA; 103896 MW; 3BF62903F644851C CRC64;

Query Match 37.8%; Score 329; DB 1; Length 925;
Best Local Similarity 43.4%; Pred. No. 4.7e-24;
Matches 69; Conservative 27; Mismatches 57; Indels 6; Gaps 3;

QY 6 CSMPLGMSKAISSAQITASSYFTN--MEATWSPSKARLHLQGRNAPQNNPKWQLQVD 65
DB 277 CNAPLGMSGRIANEQIASSTFSD--GRWTPQOSRLH--GDGNGWTPNVDNSKEYLQVD 332
QY 66 FQTKMTKVTGTTQGVKSLT--SMYKVEFLISSQDGHQWTLFPQNGKVKVFGNODSFT 123
DB 333 LRFUTMTATATQGAISRETQKGYYVKSYLEVSTNGEDMWYVRHGKHKVQFQANNDAT 392
QY 124 PVNSLDPPLLYRLRHPOSWHQIALRMEVLGCEAQQ 162
DB 393 LVLNKLHTELLTRFIRIRPQWHLGIALRLFLFCRVTD 431

RESULT 10
MFGM_PIG STANDARD; PRT; 409 AA.
AC P79385;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Lactadherin (Milk fat globule-BGF factor 8) (MFG-E8) (MFGM) (Sperm
DE surface protein SP47) (PP47).
GN MFGEB8.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
[1]
RN SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Enslin M.A.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May be involved in phospholipid binding. Zona pellucida-
CC binding protein.
CC -!- SUBCELLULAR LOCATION: Peripheral membrane protein.
CC -!- TISSUE SPECIFICITY: Mammary epithelial cell surfaces and
CC spermatozoan.
CC -!- SIMILARITY: Contains 2 EGF-like domains.
CC -!- SIMILARITY: Contains 2 F5/8 type C domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Y11683; CAA72379.1; -.
DR PIR; T11743; T11743.
DR HSSP; P00740; 1EDM.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR000421; FAS5 C.
DR InterPro; IPR008579; GalBind like.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00754; F5 F8 type C; 2.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00231; FAS5C; 2.
```

```
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS00026; EGF_3; 2.
DR PROSITE; PS01285; FAS5C_1; 2.
DR PROSITE; PS01286; FAS5C_2; 2.
DR PROSITE; PS00022; FAS5C_3; 2.
KW Glycoprotein; Repeat; EGF-like domain.
FT DOMAIN 2 41 EGF-LIKE 1.
FT DOMAIN 44 88 EGF-LIKE 2.
FT DOMAIN 91 247 F5/8 TYPE C 1.
FT DOMAIN 252 409 F5/8 TYPE C 2.
FT SITE 67 69 CELL ATTACHMENT SITE (POTENTIAL).
FT DISULFID 6 17 BY SIMILARITY.
FT DISULFID 11 29 BY SIMILARITY.
FT DISULFID 31 40 BY SIMILARITY.
FT DISULFID 91 247 BY SIMILARITY.
FT DISULFID 234 238 BY SIMILARITY.
FT DISULFID 252 409 BY SIMILARITY.
FT CARBOHYD 41 41 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 372 372 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 409 AA; 45725 MW; BOC07AF80029927A CRC64;

Query Match 37.7%; Score 328.5; DB 1; Length 409;
Best Local Similarity 39.9%; Pred. No. 2e-24;
Matches 65; Conservative 31; Mismatches 62; Indels 5; Gaps 2;

QY 1 CDLNSCSMPLGMSKAISSAQITASSYFTN--MEATWSPSKARLHLQGRNAPQNN 57
DB 247 CELSGCAEPLGLKNTIPNKQITASSFYRTWGLSAFSPFYARLDNKGKFNATQAQNS 306
QY 58 PXEWLQVDFQKTMKVTGTTQGVKSLTSMYKVEFLISSQDGHQWTLFPQNGKV--RVF 115
DB 307 AEWLQIDLGSQRTVGTITQCARDFGHIQYVAAYKVAYSDDGVSWTEYRQDGALEGRIF 366
QY 116 QNQSQSFTPVNSLDPPLLYRLRHPOSWHQIALRMEVLGC 158
DB 367 PGCLDNNSEKKNMFTPLTFVRILPVAWHNRITLRLVELLGC 409

RESULT 11
MFGM_HUMAN STANDARD; PRT; 387 AA.
AC Q08431;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Lactadherin precursor (Milk fat globule-BGF factor 8) (MFG-E8) (HMEG)
DE (Breast epithelial antigen BA46) (MFGM) [Contains: Medin].
GN MFGEB8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RC TISSUE=Breast, and Breast carcinoma;
RX MEDLINE=9131308; PubMed=8639264;
RA Couto J.R., Taylor M.R., Godwin S.G., Ceriani R.L., Peterson J.A.;
RT "Cloning and sequence analysis of human breast epithelial antigen
RT BA46 reveals an RGD cell adhesion sequence presented on an epidermal
RT growth factor-like domain".
RT DNA Cell Biol. 15:281-286(1996).
RN [2]
RN SEQUENCE OF 170-387 FROM N.A.
RC TISSUE=Mammary gland;
RX MEDLINE=91371351; PubMed=1909932;
RA Larocca D., Peterson J.A., Urrea R., Kuniyoshi J., Bistrain A.M.,
RA Ceriani R.L.;
RT "A Mr 46,000 human milk fat globule protein that is highly expressed
RT in human breast tumors contains factor VIII-like domains.";
RL Cancer Res. 51:4994-4998(1991).
RN [3]
RN PARTIAL SEQUENCE, AND CHARACTERIZATION.
```

RC TISSUE=Milk;
RX MEDLINE=98194924; PubMed=9535276;
RA Giuffrida M.G., Cavaletto M., Giunta C., Conti A.,
RA Godovac-Zimmermann J.;
RT "Isolation and characterization of full and truncated forms of human
RT breast carcinoma protein BA46 from human milk fat globule membranes.";
RL J. Protein Chem. 17:143-148(1998).
RN [4]
RP SEQUENCE OF 268-317, AND IDENTIFICATION OF MEDIN.
RX MEDLINE=99342076; PubMed=10411933;
RA Haeggqvist B., Naeslund J., Sletten K., Westermark G.T., Mucchiano G.,
RA Tjernberg L.O., Nordstedt C., Engstroem U., Westermark P.;
RT "Medin: an integral fragment of aortic smooth muscle cell-produced
RT lactadherin forms the most common human amyloid.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:8669-8674(1999).
RN [5]
RP CHARACTERIZATION.
RX MEDLINE=97405885; PubMed=9260929;
RA Taylor M.R., Couto J.R., Scallan C.D., Ceriani R.L., Peterson J.A.;
RT "Lactadherin (formerly BA46), a membrane-associated glycoprotein
RT expressed in human milk and breast carcinomas, promotes Arg-Gly-Asp
RT (RGD)-dependent cell adhesion.";
RL DNA Cell Biol. 16:861-869(1997).
RN [4]
RP FUNCTION: May be involved in phospholipid binding. Binds
CC specifically to rotavirus and inhibits its replication.
CC -!- FUNCTION: Medin is the main constituent of aortic medial amyloid.
CC -!- SUBCELLULAR LOCATION: Peripheral membrane protein.
CC -!- TISSUE SPECIFICITY: Mammary epithelial cell surfaces and aortic
CC media. Overexpressed in several carcinomas.
CC -!- PTM: MEDIN HAS A RAGGED N-TERMINUS WITH MINOR SPECIES STARTING AT
CC AMINO ACID 264 AND 273.
CC -!- SIMILARITY: Contains 1 EGF-like domain.
CC -!- SIMILARITY: Contains 2 F5/8 type C domains.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U58516; AAC50549.1; -;
CC EMBL: S56151; AAB19771.1; -;
CC PIR: A47285; A47285.
CC HSSP: P08709; 1BF9.
CC Genew: HGNC:7035; MFGE8.
CC MIN: 502381; -;
CC GO: GO:0007155; P:cell adhesion; TAG.
CC InterPro: IPR001438; EGF_1.
CC InterPro: IPR006209; EGF_like.
CC InterPro: IPR000421; FAS8 C.
CC InterPro: IPR008979; GalBind_like.
CC InterPro: IPR004210; 1BGF.
CC Pfam: PF00008; EGF_1.
CC Pfam: PF00754; F5_F8type_C; 2.
CC PRINTS: PR00010; EGFBLD.
CC SMART: SM00181; EGF; 1.
CC SMART: SM00231; FAS8C; 2.
CC PROSITE: PS00022; EGF_1; 1.
CC PROSITE: PS01185; EGF_2; 1.
CC PROSITE: PS50025; EGF_3; 1.
CC PROSITE: PS01285; FAS8C_1; 2.
CC PROSITE: PS01286; FAS8C_2; 2.
CC PROSITE: PS50022; FAS8C_3; 2.
CC KW Signal; Glycoprotein; Milk; Repeat; EGF-like domain; Amyloid.
CC SIGNAL 1 23
CC CHAIN 24 387 LACTADHERIN.
CC CHAIN 202 387 LACTADHERIN; SHORT FORM.
CC CHAIN 268 317 MEDIN.
CC DOMAIN 24 67 EGF-LIKE.
CC DOMAIN 70 225 F5/8 TYPE C 1.
CC DOMAIN 230 387 F5/8 TYPE C 2.

FT SITE 46 48 CELL ATTACHMENT SITE (POTENTIAL).
FT DISULFID 37 38 BY SIMILARITY.
FT DISULFID 52 55 BY SIMILARITY.
FT DISULFID 57 66 BY SIMILARITY.
FT DISULFID 70 225 BY SIMILARITY.
FT DISULFID 212 216 BY SIMILARITY.
FT DISULFID 230 387 BY SIMILARITY.
FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 325 325 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 329 329 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 387 AA; 43123 MW; 25E6571DEC83782D CEC64;
Query Match 37.6%; Score 327.5; DB 1; Length 387;
Best Local Similarity 40.2%; Pred. No. 2.3e-24;
Matches 66; Conservative 35; Mismatches 56; Indels 7; Gaps 3;
QY 1 CDLNSCSMPLGMEKASISDAQITASSYF---TNMFATWSPSKARLHLQGRSNARPPQVN 56
Db 225 CELNGCANPLGLKKNIPDKQITASSSYKWTGLHLP-SWNPSTYARLDKQGNFNAWAGSY 283
QY 57 NPKEWLQVDFQTKMKTGVTITQGVKSLTSMYKFEISSLSSQDGHQWTLFF--QNGKVKV 114
Db 284 GNDQWLQVLDLGSKEVTGIITQGARNFQSVQFVASYKVAYNSDANSANWTEYQDPRTGSKI 343
QY 115 FQGNQDSFTPVNSLDPLLTLYRIHPOSVHQAIRMEVLGC 158
Db 344 PFGNWDNHSKKNLFFETPILARYVRIPLFVAWHNRILRLLELGC 387
RESULT 12
NRP2_HUMAN
ID NRP2_HUMAN STANDARD; PRT; 931 AA.
AC 060462; O14820; O14821;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuropilin-2 precursor (Vascular endothelial cell growth factor 165
DE receptor 2).
GN NRP2 OR VSGF165R2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS A0 AND A17).
RX MEDLINE=97473888; PubMed=9331348;
RA Chen H., Chedotal A., He Z.-G., Goodman C.S., Tessier-Lavigne M.;
RT "Neuropilin-2, a novel member of the neuropilin family, is a high
RT affinity receptor for the semaphorins Sema E and Sema IV but not Sema
RT III.";
RL Neuron 19:547-559(1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM A22).
RC TISSUE=Breast;
RX MEDLINE=98188099; PubMed=9529250;
RA Soker S., Takashima S., Miao H.-Q., Neufeld G., Klagsbrun M.;
RT "Neuropilin-1 is expressed by endothelial and tumor cells as an
RT isoform-specific receptor for vascular endothelial growth factor.";
RL Cell 92:735-745(1998).
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=20309748; PubMed=10748121;
RA Gluzman-Poltorak Z., Cohen T., Herzog Y., Neufeld G.;
RT "Neuropilin-2 and neuropilin-1 are receptors for the 165-amino acid
RT form of vascular endothelial growth factor (VEGF) and of placenta
RT growth factor-2, but only neuropilin-2 functions as a receptor for
RT the 145-amino acid form of VEGF";
RL J. Biol. Chem. 275:18040-18045(2000).
CC -!- FUNCTION: High affinity receptor for semaphorins 3C, 3F, VEGF-165
CC and VEGF-145 isoforms of VEGF, and the PLGF-2 isoform of PGF.
CC -!- SUBUNIT: Neuropilin-2 probably forms a heteromeric complex with
CC neuropilin-1 in order to be a functional semaphorin 3C receptor.

```
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=A22;
CC IsoId=060462-1; Sequence=Displayed;
CC Name=A0;
CC IsoId=060462-2; Sequence=VSP_004342;
CC Name=A17;
CC IsoId=060462-3; Sequence=VSP_004341;
CC -!- SIMILARITY: Belongs to the neuropilin family.
CC -!- SIMILARITY: Contains 2 CUB domains.
CC -!- SIMILARITY: Contains 2 F5/8 type C domains.
CC -!- SIMILARITY: Contains 1 MAM domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; AF022859; AAC51788.1; -
CC DR EMBL; AF022850; AAC51789.1; -
CC DR EMBL; AF016098; AAC12922.1; -
CC DR HSPF; P12259.1CZT.
CC DR Genew; HGNC:8005; NRP2.
CC MIM; 602070; -
CC DR GO; GO:0005624; C:membrane fraction; TAS.
CC DR GO; GO:0004872; F:receptor activity; TAS.
CC DR GO; GO:0005021; F:vascular endothelial growth factor receptor. . . ; TAS.
CC DR GO; GO:0007411; P:axon guidance; TAS.
CC InterPro; IPR000859; CUB.
CC DR InterPro; IPR000421; FA58_C.
CC DR InterPro; IPR008979; Gal_Bind_Like.
CC DR InterPro; IPR000998; MAM_domain.
CC Pfam; PF00431; CUB; 2.
CC Pfam; PF00754; F5_F8_type_C; 2.
CC Pfam; PF00629; MAM; 1.
CC PRINTS; PR00020; MAMDOMAIN.
CC DR SMART; SM00042; CUB; 2.
CC DR SMART; SM00231; FA58C; 2.
CC DR SMART; SM00137; MAM; 1.
CC DR PROSITE; PS01180; CUB; 2.
CC DR PROSITE; PS01285; FA58C_1; 2.
CC DR PROSITE; PS01286; FA58C_2; 2.
CC DR PROSITE; PS00022; FA58C_3; 2.
CC DR PROSITE; PS00060; MAM_2; 1.
CC Transmembrane; Glycoprotein; Neurone; Signal; Repeat; Receptor;
KW Alternative splicing.
FT SIGNAL 1 20 OR 22 (POTENTIAL).
FT CHAIN 21 931 NEUROFILIN-2.
FT DOMAIN 21 864 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 865 889 POTENTIAL.
FT DOMAIN 890 931 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 28 142 CUB 1.
FT DOMAIN 149 267 CUB 2.
FT DOMAIN 277 427 F5/8 TYPE C 1.
FT DOMAIN 434 592 F5/8 TYPE C 2.
FT DOMAIN 642 802 MAM.
FT DOMAIN 671 674 POLY-SER.
FT DISULFID 28 55 BY SIMILARITY.
FT DISULFID 83 105 BY SIMILARITY.
FT DISULFID 149 175 BY SIMILARITY.
FT DISULFID 208 230 BY SIMILARITY.
FT DISULFID 277 427 BY SIMILARITY.
FT DISULFID 434 592 BY SIMILARITY.
FT CARBOHYD 152 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 629 629 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 839 839 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLC 809 813 Missing (in isoform A17).
FT /FTId=VSP_004341.
```

```
FT VARSPLC 809 830 Missing (in isoform A0).
FT /FTId=VSP_004342.
FT CONFLICT 602 602 E -> K (IN REF. 1).
FT SEQUENCE 931 AA; 104830 MW; 270CBAE69A0A797C CRC64;
Query Match 37.5%; Score 327; DB 1; Length 931;
Best Local Similarity 42.1%; Pred. No. 7.4e-24;
Matches 67; Conservative 30; Mismatches 56; Indels 6; Gaps 3;
QY 6 CSMPLGMSKAISSDAQITASSYFTNMATWSSKARLHQLQGRSNARPOVNNPKEWLQVD 65
Db 277 CNVPLGMSGRIANEQISASTYSD--GRWTPQOSRLH--GDDNGWTNLDSNKEYLQVD 332
QY 66 FQTKMKVGTGVTQGVKSLT--SMYVKFLISSQDGHQWTLFFQNGKVKVQFGNQDSFT 123
Db 333 LRLFTMLTAIATQGAISRETQNGYVYKYLEVSTNGEDVMVYRGRKHKVQFQANNDAT 392
QY 124 PVVNSIDPPLRLRYLRIPQSVWVHOIALRMEVLGCEAOD 162
Db 393 VVINKLHAPLLTRFVRIRPQTWHSGIALRLLELFGCRVTD 431
RESULT 13
NRP2 MOUSE
ID_NRP2_MOUSE STANDARD; PRT: 931 AA
AC O35375; O35373; O35374; O35376; O35377; O35378;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Neuropilin-2 precursor (Vascular endothelial cell growth factor 165
DE Receptor 2).
GN NRP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A. (ISOFORMS A0; A17; A22; A5; B0 AND B5).
RC STRAIN=BALB/C.
RX MEDLINE=97470888; PubMed=9331348;
RA Chen H., Chedotal A., He Z.-G., Goodman C.S., Tessier-Lavigne M.;
RT "Neuropilin-2, a novel member of the neuropilin family, is a high
RT affinity receptor for the semaphorins Sema E and Sema IV but not Sema
RT III.";
RL Neuron 19:547-559(1997).
CC -!- FUNCTION: High affinity receptor for semaphorins 3C, 3F, VEGF-165
CC and VEGF-145 isoforms of VEGF, and the p16F-2 isoform of PGF.
CC -!- SUBUNIT: Neuropilin-2 probably forms a heteromeric complex with
CC neuropilin-1 in order to be a functional semaphorin E receptor.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=6;
CC Name=A22;
CC IsoId=O35375-1; Sequence=Displayed;
CC Name=A0;
CC IsoId=O35375-2; Sequence=VSP_004344;
CC Name=A5;
CC IsoId=O35375-3; Sequence=VSP_004345;
CC Name=A17;
CC IsoId=O35375-4; Sequence=VSP_004343;
CC Name=B0;
CC IsoId=O35375-5; Sequence=VSP_004346;
CC Name=B5;
CC IsoId=O35375-6; Sequence=VSP_004347;
CC -!- TISSUE SPECIFICITY: Expressed in developing cns, PNS and in some
CC nonneural tissues including limb buds, developing bones, muscles,
CC intestinal epithelium, kidney, lung and submandibular gland.
CC -!- DEVELOPMENTAL STAGE: The expression pattern is very dynamic and is
CC developmentally regulated.
CC -!- SIMILARITY: Belongs to the neuropilin family.
CC -!- SIMILARITY: Contains 2 CUB domains.
CC -!- SIMILARITY: Contains 2 F5/8 type C domains.
CC -!- SIMILARITY: Contains 1 MAM domain.
```

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>)
 CC or send an email to license@isb-sib.ch.
 CC -----
 DR EMBL; AF022856; AAC53379.1; -
 DR EMBL; AF022854; AAC53377.1; -
 DR EMBL; AF022855; AAC53378.1; -
 DR EMBL; AF022857; AAC53380.1; -
 DR EMBL; AF022858; AAC53381.1; -
 DR EMBL; AF022861; AAC53382.1; -
 DR HSP; P12259; ICZT.
 DR MGD; MGI:1100492; Nrp2.
 DR InterPro; IPR000859; CUB.
 DR InterPro; IPR000421; FA58_C.
 DR InterPro; IPR008979; Gal_Bind_like.
 DR InterPro; IPR000998; MAM_domain.
 DR Pfam; PF00431; CUB; 2.
 DR Pfam; PF00754; F5_F8_type_C; 2.
 DR PRINTS; PR00020; MAMDOMAIN.
 DR SMART; SM00042; CUB; 2.
 DR SMART; SM00231; FA58C; 2.
 DR SMART; SM00137; MAM; 1.
 DR PROSITE; PS01180; CUB; 2.
 DR PROSITE; PS01285; FA58C_1; 2.
 DR PROSITE; PS01286; FA58C_2; 2.
 DR PROSITE; PS00022; FA58C_3; 2.
 DR PROSITE; PS50060; MAM_2; 1.
 DR Transmembrane; Glycoprotein; Neurone; Signal; Repeat; Receptor;
 KW Alternative splicing.
 FT SIGNAL 1 20
 FT CHAIN 21 931
 FT DOMAIN 21 864
 FT TRANSMEM 865 889
 FT DOMAIN 890 931
 FT DOMAIN 28 142
 FT DOMAIN 149 267
 FT DOMAIN 277 427
 FT DOMAIN 434 592
 FT DOMAIN 642 802
 FT DOMAIN 838 845
 FT DISULFID 28 55
 FT DISULFID 83 105
 FT DISULFID 149 175
 FT DISULFID 208 230
 FT DISULFID 277 427
 FT DISULFID 434 592
 FT CARBOHYD 152 157
 FT CARBOHYD 157 157
 FT CARBOHYD 629 629
 FT CARBOHYD 839 839
 FT VARSPLIC 809 813
 FT VARSPLIC 809 830
 FT VARSPLIC 814 830
 FT VARSPLIC 810 931
 ZDFKSWLYTHGEGYDEIDDEYEGDWSNSSSTSGAGDP
 SSGKEKSWLYTHGEGYDEIDDEYEGDWSNSSSTSGAGDP
 CSYGLSRCTLTENLYFELGDKHKVKNKQCCSEA
 -> GTLPFGTEPTVDTPVQPIPAYWYNNAGGAVLVAS
 VVALVHRYFRVAAKTDHSITYKTSHTNGAPLAVPT
 LTKLEQERSHC (in isoform B0).
 /FTid=VSP_004346
 VDIPTFHGEGYDEIDDEYEGDWSNSSSTSGAGDPSSGK
 EKSWLYTHGEGYDEIDDEYEGDWSNSSSTSGAGDPSSGK
 GLSRCTLTENLYFELGDKHKVKNKQCCSEA -> G
 GTLPFGTEPTVDTPVQPIPAYWYNNAGGAVLVASVVL

FT ALVLHRYFRVAAKTDHSITYKTSHTNGAPLAVPTLTI
 FT KLEQERSHC (in isoform B5).
 FT /FTid=VSP_004347.
 FT CONFLICT 786 786
 FT G -> I (IN REF. 1; AAC53380/AAC53381).
 SQ SEQUENCE 931 AA; 104558 MW; 76F2443F411D2F63 CRC64;
 Query Match 37.5%; Score 327; DB 1; Length 931;
 Best Local Similarity 42.1%; Pred. No. 7.4e-24;
 Matches 67; Conservative 30; Mismatches 56; Indels 6; Gaps 3;
 QY 6 CSMPLGMSKASDAQITASSYFTNMFATWSPSKARHLQGRSNARPOVANNPKWQLQVD 65
 DB 277 CNVPLGMSGRIANEQISASTFSD--GRWTPQOSRLH--GDDNGWTENLDSNKKEYLQVD 332
 QY 66 FOKTKVKTGVTQTGVKSLLT--SMYVKEFLISSQDGHQWTLFFQNGKVKVQFQGNQDSFT 123
 DB 333 LFLFLMLTAIATQGAISRETQKGYVYSKLEVTNGEDMMVYRHGKHKIFQANNDATE 392
 QY 124 PVVNSLDPLLTLYRIHQPQSWHQAIALRMEVLGCEAOD 162
 DB 393 VVINKLHMLLTFRFIRIRPQTHLGLIALRLFLFCGRVTD 431
 RESULT 14
 MFCM BOVIN
 ID MFCM BOVIN STANDARD; PRT; 427 AA.
 AC Q95114; P79344; Q27959;
 DT 01-NOV-1997 (Rel. 35; Created)
 DT 01-NOV-1997 (Rel. 35; Last sequence update)
 DT 15-MAR-2004 (Rel. 43; Last annotation update)
 DE Lactadherin precursor (Milk fat globule-EGF factor 8) (MFG-E8)
 DE (MGP57/53) (PAS-6/PAS-7 glycoprotein) (MFCM) (Sperm surface protein
 DE SP47) (BP47) (Components 15/16).
 GN MFC8.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]_TaxID=9913;
 RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CARBOHYDRATE-LINKAGE SITES.
 RC STRAIN=Holstein; TISSUE=Mammary gland;
 RX MEDLINE=97008954; PubMed=8856064;
 RA Hvarregaard J., Andersen M.H., Berglund L., Rasmussen J.T.,
 RA Petersen T.E.;
 RT "Characterization of glycoprotein PAS-6/7 from membranes of bovine
 RT milk fat globules.";
 RL Eur. J. Biochem. 240:628-636 (1996).
 RN [2]
 RP SEQUENCE OF 19-427 FROM N.A.
 RC TISSUE=Mammary gland;
 RX MEDLINE=96125736; PubMed=8541316;
 RA Aoki N., Kishi M., Taniguchi Y., Adachi T., Nakamura R.,
 RA Matsuda T.;
 RT "Molecular cloning of glycoprotein antigens MGP57/53 recognized by
 RT monoclonal antibodies raised against bovine milk fat globule
 RT membrane.";
 RL Biochim. Biophys. Acta 1245:385-391 (1995).
 RN [3]
 RP SEQUENCE OF 19-427 FROM N.A.
 RC TISSUE=Testis;
 RA Ensalin M.A.;
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 140-146; 174-187; 233-246 AND 422-427.
 RC TISSUE=Milk;
 RX MEDLINE=93250576; PubMed=8485470;
 RA Mather I.H., Banghart L.R., Lane W.S.;
 RT "The major fat-globule membrane proteins, bovine components 15/16 and
 RT guinea-pig GP 55, are homologous to MGP-E8, a murine glycoprotein
 RT containing epidermal growth factor-like and factor V/VIII-like
 RT sequences.";
 RL Biochem. Mol. Biol. Int. 29:545-554 (1993).

CC -!- FUNCTION: Probably associates with phospholipids on the surface of
 CC mammary epithelial cells and milk fat globules. Zona pellucida-
 CC binding protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=Long;
 CC isoId=Q95114-1; Sequence=Displayed;
 CC Name=Short;
 CC isoId=Q95114-2; Sequence=VSP_001398;
 CC -!- TISSUE SPECIFICITY: Milk and spermatozoan.
 CC -!- PTM: THE 2 O-LINKED GLYCANS CONSTIT OF GAL, GLCNAC AND FUC, WITH
 CC PROBABLY FUC AS REDUCING TERMINAL SUGAR.
 CC -!- SIMILARITY: Contains 2 EGF-like domains.
 CC -!- SIMILARITY: Contains 2 F5/8 type C domains.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; X91895; CAA62997.1; -;
 CC EMBL; S80643; AAB35894.2; -;
 CC EMBL; Y11719; CAA72406.1; -;
 CC PIR; S74211; S74211.
 CC HSP; P00740; I1XA.
 CC InterPro; IPR006209; EGF like.
 CC InterPro; IPR000421; FAS8_C.
 CC InterPro; IPR008979; Gal_Bind_like.
 CC InterPro; IPR006210; IEGF.
 CC Pfam; PF00008; EGF; 2.
 CC Pfam; PF00754; F5_F8_type_C; 2.
 CC SMART; SM00181; EGF; 2.
 CC SMART; SM00231; FAS8C; 2.
 CC PROSITE; PS00022; EGF_1; 2.
 CC PROSITE; PS01186; EGF_2; 2.
 CC PROSITE; PS00026; EGF_3; 2.
 CC PROSITE; PS01285; FAS8C_1; 2.
 CC PROSITE; PS01286; FAS8C_2; 2.
 CC PROSITE; PS00022; FAS8C_3; 2.
 CC Signal; Glycoprotein; Milk; Repeat; EGF-like domain;
 KW Alternative splicing.
 KW
 FT SIGNAL 1
 FT CHAIN 19 427
 FT LACTADHERIN.
 FT EGF-LIKE 1.
 FT EGF-LIKE 2.
 FT F5/8 TYPE C 1.
 FT F5/8 TYPE C 2.
 FT F5/8 TYPE C 2.
 FT CELL ATTACHMENT SITE (POTENTIAL).
 FT BY SIMILARITY.
 FT BY SIMILARITY.
 FT BY SIMILARITY.
 FT BY SIMILARITY.
 FT BY SIMILARITY.
 FT BY SIMILARITY.
 FT O-LINKED (FUC...) (IN PAS-6).
 FT O-LINKED (FUC...) (IN PAS-7).
 FT N-LINKED (GLCNAC...) (HYBRID)
 FT (IN PAS-6 AND PAS-7).
 FT N-LINKED (GLCNAC...) (HIGH MANNOSE)
 FT (IN PAS-6).
 FT Missing (in isoform Short).
 FT VARSPLIC 169 221
 FT A -> F (IN REF. 1).
 FT L -> Q (IN REF. 1).
 FT CONFLICT 28 28
 FT SEQUENCE 427 AA; 47411 MW; 4CBBE3A1DC4EB24 CRC64;
 SQ
 Query Match 37.3%; Score 324.5; DB 1; Length 427;

Best Local Similarity 39.3%; Pred. No. 5.1e-24;
 Matches 64; Conservative 29; Mismatches 65; Indels 5; Gaps 2;
 QY 1 CDLNSCMPILGMSKAISSDAQTASSYFTN---MFATWSPSKARLHLCGRSNARWPOVNN 57
 DB 265 CELNGCTEPLGLKNDTIPKQITASSYKRWGLSAPFWPPYARLDNQKRFNAQTNS 324
 QY 58 PREWLQVDFQKTMKVTGVTQTQGVKSLTSMYKFLISSQDGHOWTLFFQNG--KVKYF 115
 DB 325 ASEWLQIDLSGQKRVGTGIITQARDFGHIOYVAARVAYGDDGVTWTEYKDPGASESKIP 384
 QY 116 QGNQDSFTFVNSLDPPLTRVLRTHPQSWVHQIALRMEVLGC 158
 DB 385 PGNDNNSHKKIFPPFOARFVRIOQVAWHNRITLURVELGC 427
 RESULT 15
 NRPI_CHICK
 ID NRPI_CHICK STANDARD; PRT; 914 AA.
 AC P79735; AC
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DE 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Neurophilin-1 precursor (A5 protein).
 GN NRPI OR NRP.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=White Leghorn; TISSUE=Embryonic brain;
 RX MEDLINE=95324761; PubMed=7601310;
 RA Takagi S., Kasuya Y., Shimizu M., Matsuura T., Tsuboi M., Kawakami A.,
 RA Fujisawa H.;
 RT "Expression of a cell adhesion molecule, neurophilin, in the
 RT developing chick nervous system.";
 RL Dev. Biol. 170:207-222(1995).
 CC -!- FUNCTION: Receptor involved in the development of the
 CC cardiovascular system, in angiogenesis, in the formation of
 CC certain neuronal circuits and in organogenesis outside the nervous
 CC system. It mediates the chemorepulsant activity of semaphorins (By
 CC similarity). Seems to have calcium-independent cell adhesion
 CC properties.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: Developing nervous system; optic tectum
 CC (layers D and E of SGFS), amacrine cells of retina, neurites of
 CC dorsal root ganglia. Also expressed in nonneuronal cells, e.g.
 CC blood vessels in the entire embryo.
 CC -!- SIMILARITY: Belongs to the neurophilin family.
 CC -!- SIMILARITY: Contains 2 CUB domains.
 CC -!- SIMILARITY: Contains 2 F5/8 type C domains.
 CC -!- SIMILARITY: Contains 1 MAM domain.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; D45416; BAA08256.1; -;
 CC HSP; P12259; 1CZT.
 CC InterPro; IPR000859; CUB.
 CC InterPro; IPR000421; FAS8_C.
 CC InterPro; IPR008979; Gal_Bind_like.
 CC InterPro; IPR000998; MAM_domain.
 CC Pfam; PF00431; CUB; 2.
 CC Pfam; PF00754; F5_F8_type_C; 2.
 CC Pfam; PF00629; MAM; 1.
 CC PRINTS; PRO0020; MAMDOMAIN.
 DR

DR SMART; SM00042; CUB; 2.
 DR SMART; SM00231; FA58C; 2.
 DR SMART; SM00137; MAM; 1.
 DR PROSITE; PS01180; CUB; 2.
 DR PROSITE; PS01285; FA58C_1; 2.
 DR PROSITE; PS01286; FA58C_2; 2.
 DR PROSITE; PS00022; FA58C_3; 2.
 DR PROSITE; PS00740; MAM_1; 1.
 DR PROSITE; PS00060; MAM_2; 1.
 KW Angiogenesis; Transmembrane; Glycoprotein; Neurone; Signal; Repeat;
 KW Receptor; Cell adhesion.
 FT SIGNAL 1 18
 FT CHAIN 19 914
 FT DOMAIN 20 847
 FT TRANSMEM 848 870
 FT DOMAIN 871 914
 FT DOMAIN 25 139
 FT DOMAIN 145 263
 FT DOMAIN 273 422
 FT DOMAIN 429 581
 FT DOMAIN 536 801
 FT DISULFID 25 52
 FT DISULFID 80 102
 FT DISULFID 145 171
 FT DISULFID 204 226
 FT DISULFID 273 422
 FT DISULFID 429 581
 SQ SEQUENCE 914 AA; 102480 MW; DD2EE6D6F0CBB68C CRC64;
 Query Match 31.6%; Score 275.5; DB 1; Length 914;
 Best Local Similarity 37.7%; Pred. No. 7.2e-19;
 Matches 60; Conservative 24; Mismatches 68; Indels 7; Gaps 3;
 QY 6 CSMPLGMSKAISSAQITASSYFTNMFATWSPKARLHLOGRSNARPPQVNNPKWLQVD 65
 Db 273 CMEPLGMSGSIHSDQITVSSQYS---AIWSSERSRLNYP--ENGWTPGEDSVREWIQVD.327
 QY 66 FQKTMKVTGVTQGV--KSLITSMVYKFEFLISSODGHQWTLRFONGKVKVFGQNDST 123
 Db 328 LGLRFVSGIGTQGAISKETKKEYLKYRVYDVSSNGEDWITLKEGNKPVVFGQNSNPTD 387
 QY 124 PVVNSLDPPLLTRYLRHPQSWHQAIALRMEVLGCEAQD 162
 Db 388 VVYRPFPKPVLTFRVRIKPVSWENGVSRLRFEVYGCKITD 426

Search completed: September 29, 2004, 16:40:02
 Job time : 14 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model
Run on: September 29, 2004, 16:34:18 ; Search time 41 Seconds
(without alignments)
1262.073 Million cell updates/sec

Title: US-10-049-399A-1_COPY_2169_2332
Perfect score: 871
Sequence: 1 CDLNSCMPGMSKALSDA.....WVHQIALRMEVLGCRQDIY 164

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	871	100.0	216	4	Q14286
2	736	84.5	2343	6	O18806
3	731	83.9	2343	6	O62730
4	618	71.0	2258	11	Q7TN96
5	568	65.2	1377	13	Q804X3
6	465	53.4	1639	13	Q804W6
7	405	45.5	1460	13	Q7SZN0
8	402	44.2	745	13	Q804X4
9	390	44.8	2183	11	Q88783
10	385	44.2	2102	11	Q7TPK2
11	365.5	42.1	480	4	Q8N610
12	366.5	42.1	480	4	O4385A
13	365.5	42.0	407	13	Q8AIE0
14	365.5	42.0	2119	13	Q90X47
15	357.5	41.0	426	11	Q9WTS3
16	357.5	41.0	463	11	Q9RIX9

17	357.5	41.0	470	11	Q8C4U8	Q8c4u8 mus musculu
18	357.5	41.0	480	11	Q8CBP7	Q8cbp7 mus musculu
19	357.5	41.0	480	11	O35474	O35474 mus musculu
20	354.5	40.7	1802	13	Q804W5	Q804w5 fugu rubrip
21	330	37.9	384	11	Q8C8K0	Q8c8k0 mus musculu
22	327	37.5	555	4	Q9H2E2	Q9h2e2 homo sapien
23	327	37.5	901	4	Q9H2E4	Q9h2e4 homo sapien
24	327	37.5	901	4	Q9H2D5	Q9h2d5 homo sapien
25	327	37.5	906	4	Q9H2D4	Q9h2d4 homo sapien
26	327	37.5	906	4	Q9H2E3	Q9h2e3 homo sapien
27	327	37.5	926	11	Q8QZT7	Q8qzt7 mus musculu
28	327	37.5	931	4	Q7Z3T9	Q7z3t9 homo sapien
29	323.5	37.1	312	4	Q7Z3D2	Q7z3d2 homo sapien
30	312	35.8	905	13	Q800I4	Q800i4 gallus gall
31	311	35.7	919	13	Q8UVR0	Q8uvr0 gallus gall
32	311	35.7	936	13	Q8UVQ9	Q8uvq9 gallus gall
33	306.5	35.2	743	4	Q8N6M4	Q8n6m4 homo sapien
34	306.5	35.2	775	4	Q8TDX2	Q8tdx2 homo sapien
35	306.5	35.2	775	4	Q86PD2	Q86pd2 homo sapien
36	299.5	34.4	769	11	Q91ZV2	Q91zv2 rattus norv
37	294.5	33.8	602	11	Q8BK14	Q8bki4 mus musculu
38	294.5	33.8	769	11	Q91ZV3	Q91zv3 mus musculu
39	285.5	32.8	524	4	Q8N8Z6	Q8n8z6 homo sapien
40	285.5	32.8	539	4	Q8IYK5	Q8iyk5 homo sapien
41	283.5	32.5	858	5	O76470	O76470 lytechinus
42	278.5	32.0	923	13	Q8QFX6	Q8qfx6 brachydanio
43	278.5	32.0	923	13	Q8AXP1	Q8axp1 brachydanio
44	273	31.3	51	4	Q9UQ05	Q9uqg5 homo sapien
45	272	31.2	335	4	Q9BTL9	Q9btl9 homo sapien

ALIGNMENTS

RESULT 1

Q14286 PRELIMINARY; PRT; 216 AA.

AC Q14286; (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DE 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Coagulation factor VIII associated protein B (Coagulation factor VIII, procoagulant component) (Hemophilia A).
GN F8B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93052386; PubMed=1427887;
RA Levinson B., Kenrick S., Gamel P., Fisher K., Gitschler J.;
RT "Evidence for a third transcript from the human factor VIII gene."
RL Genomics 14:585-589(1992).

[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
CC -!- SIMILARITY: CONTAINS 1 FS/8 TYPE C DOMAIN.
EMBL; M90707; AAAS8466.1; -.
DR EMBL; BC022513; AAH22513.1; -.
DR PIR; A44258; A44258.
DR HSSP; P00431; LCFG.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR000421; FAS8C.
DR InterPro; IPR008979; GalBind-like.
DR Pfam; PF00754; F5_F8 type C; 2.
DR SMART; SM00231; FAS8C; 1.
DR PROSITE; PS01285; FAS8C; 1.
DR PROSITE; PS01286; FAS8C; 2.
DR PROSITE; PS50022; FAS8C; 2.
SQ SEQUENCE 216 AA; 24641 MW; 6C82D4F89E35A376 CRC64;

```

Query Match
Best Local Similarity 100.0%; Score 871; DB 4; Length 216;
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDLNSCMPLGMSKAISSDAQITASSYFTNMFWATWSPSKARLHLQGRSNARWPQVNNPKE 60
DB 53 CDLNSCMPLGMSKAISSDAQITASSYFTNMFWATWSPSKARLHLQGRSNARWPQVNNPKE 112

QY 61 WLQVDFQKTMKVTGTTQGVKSLTSMYKFEFLISSQDGHQWTLFPQNGKVKVFGNQD 120
DB 113 WLQVDFQKTMKVTGTTQGVKSLTSMYKFEFLISSQDGHQWTLFPQNGKVKVFGNQD 172

QY 121 SFTPVNSLDPPLTLRYLRHPQSVWHQIALRMEVLGCEAQDLY 164
DB 173 SFTPVNSLDPPLTLRYLRHPQSVWHQIALRMEVLGCEAQDLY 216

RESULT 2
OL8806 PRELIMINARY; PRT; 2343 AA.
AC OL8806;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Factor VIII.
GN F8.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
EN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Cameron C., Nottley C., Hoyle S., McGlynn L., Hough C., Kamisue S.,
RA Giles A., Lilliecrap D.;
RT "The canine factor VIII cDNA and 5' flanking sequence.";
RL Submitted (NCV-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 2 FS/8 TYPE C DOMAINS.
DR EMBL; AF016234; AB87412.1; -.
DR HSSP; P00451; 1CFG.
DR GO; GO:0005507; F: copper ion binding; IEA.
DR GO; GO:0007155; P: cell adhesion; IEA.
DR InterPro; IPR001117; Cu-oxidase.
DR InterPro; IPR008972; Cupredoxin.
DR InterPro; IPR000421; FA58_C.
DR Pfam; PF00754; F5_F8 type C; 2.
DR SMART; SM00231; FA58C_2; 2.
DR PROSITE; PS01285; FA58C_1; 2.
DR PROSITE; PS01286; FA58C_2; 2.
DR PROSITE; PS50022; FA58C_3; 2.
DR PROSITE; PS50022; FA58C_3; 2.
DR PROSITE; PS00079; MULTICOPPER OXIDASE1; 3.
SQ SEQUENCE 2343 AA; 265829 MW; A854FAE571C3B399 CRC64;

Query Match
Best Local Similarity 84.5%; Score 736; DB 6; Length 2343;
Matches 134; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

QY 1 CDLNSCMPLGMSKAISSDAQITASSYFTNMFWATWSPSKARLHLQGRSNARWPQVNNPKE 60
DB 2180 CDLNSCMPLGMSKAISSDAQITASSYFTNMFWATWSPSKARLHLQGRSNARWPQVNNPKE 2239

QY 61 WLQVDFQKTMKVTGTTQGVKSLTSMYKFEFLISSQDGHQWTLFPQNGKVKVFGNQD 120
DB 2240 WLQVDFQKTMKVTGTTQGVKSLTSMYKFEFLISSQDGHQWTLFPQNGKVKVFGNQD 2299

QY 121 SFTPVNSLDPPLTLRYLRHPQSVWHQIALRMEVLGCEAQ 161
DB 2300 SFTPVNSLDPPLTLRYLRHPQSVWHQIALRMEVLGCEAQ 2340

Query Match
Best Local Similarity 83.2%; Pred. No. 3.5e-66;
Matches 134; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

QY 1 CDLNSCMPLGMSKAISSDAQITASSYFTNMFWATWSPSKARLHLQGRSNARWPQVNNPKE 60
DB 2180 CDLNSCMPLGMSKAISSDAQITASSYFTNMFWATWSPSKARLHLQGRSNARWPQVNNPKE 2239

QY 61 WLQVDFQKTMKVTGTTQGVKSLTSMYKFEFLISSQDGHQWTLFPQNGKVKVFGNQD 120
DB 2240 WLQVDFQKTMKVTGTTQGVKSLTSMYKFEFLISSQDGHQWTLFPQNGKVKVFGNQD 2299

QY 121 SFTPVNSLDPPLTLRYLRHPQSVWHQIALRMEVLGCEAQ 161
DB 2300 SFTPVNSLDPPLTLRYLRHPQSVWHQIALRMEVLGCEAQ 2340

```

```

RESULT 3
O62730 PRELIMINARY; PRT; 2343 AA.
AC O62730;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Factor VIII.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
EN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney, and Spleen;
RA Gordy P.W., Bowen R.A.;
RT "Characterization of the canine factor VIII cDNA.";
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 2 FS/8 TYPE C DOMAINS.
DR EMBL; AF049489; AAC05384.1; -.
DR HSSP; P00451; 1CFG.
DR GO; GO:0005507; F: copper ion binding; IEA.
DR GO; GO:0007155; P: cell adhesion; IEA.
DR InterPro; IPR001117; Cu-oxidase.
DR InterPro; IPR008972; Cupredoxin.
DR InterPro; IPR000421; FA58_C.
DR Pfam; PF00754; F5_F8 type C; 2.
DR SMART; SM00231; FA58C_2; 2.
DR PROSITE; PS01285; FA58C_1; 2.
DR PROSITE; PS01286; FA58C_2; 2.
DR PROSITE; PS50022; FA58C_3; 2.
DR PROSITE; PS50022; FA58C_3; 2.
DR PROSITE; PS00079; MULTICOPPER OXIDASE1; 3.
SQ SEQUENCE 2343 AA; 265613 MW; F612D74ADAADD99 CRC64;

Query Match
Best Local Similarity 83.9%; Score 731; DB 6; Length 2343;
Matches 133; Conservative 14; Mismatches 14; Indels 0; Gaps 0;

QY 1 CDLNSCMPLGMSKAISSDAQITASSYFTNMFWATWSPSKARLHLQGRSNARWPQVNNPKE 60
DB 2180 CDLNSCMPLGMSKAISSDAQITASSYFTNMFWATWSPSKARLHLQGRSNARWPQVNNPKE 2239

QY 61 WLQVDFQKTMKVTGTTQGVKSLTSMYKFEFLISSQDGHQWTLFPQNGKVKVFGNQD 120
DB 2240 WLQVDFQKTMKVTGTTQGVKSLTSMYKFEFLISSQDGHQWTLFPQNGKVKVFGNQD 2299

QY 121 SFTPVNSLDPPLTLRYLRHPQSVWHQIALRMEVLGCEAQ 161
DB 2300 SFTPVNSLDPPLTLRYLRHPQSVWHQIALRMEVLGCEAQ 2340

RESULT 4
Q7TN96 PRELIMINARY; PRT; 2258 AA.
AC Q7TN96;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Factor VIII.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
EN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Liver;
RA Watzka M., Geisen C., Seifried E., Oldenburg J.;
RT "Sequence of the rat factor VIII cDNA.";
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY362193; AAQ21580.1; -.
DR EMBL; AY362193; AAQ21580.1; -.
SQ SEQUENCE 2258 AA; 251299 MW; 13AF91C788059B1D CRC64;

```

Query Match 71.0%; Score 618; DB 11; Length 2258;
 Best Local Similarity 68.7%; Pred. No. 4.5e-54;
 Matches 112; Conservative 23; Mismatches 28; Indels 0; Gaps 0;

QY 1 CDLNSCMPGLMESKASDAQITASSYFTNNFATWSPSKARHLQGRSNARWPOVNNPKE 60
 DB 2095 CDLNSCAPLGMESGWSIDQVTQVASSLSLTFSAWPPALARHLRGANARWQVNDPTQ 2154

QY 61 WLQVDFQKTMKVTGVTQGVKSLTSMYVKEFLISSQDGHQWTLFPQNGKVKVQFQNGD 120
 DB 2155 WLQVDFQKTMKVTGVTQGVKSLTSMYVKEFLISSQDGHQWTLFPQNGKVKVQFQNGD 2214

QY 121 SFTPVNSLDPELLTRYLRHQPQSWHQAIALRMEVLGCEAQLD 163
 DB 2215 ASTPVNSLHPPTRYLRHQPQSWHQAIALRMEVLGCEAQLD 2257

RESULT 5
 ID Q804X3 PRELIMINARY; PRT; 1377 AA.
 AC Q804X3;
 DT 01-JUN-2003 (TRENBLrel. 24, Created)
 DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Coagulation factor VIII precursor (Fragment).
 GN F8.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Davidson C.J., Hirt R.P., Lal K., Snell P., Elgar G.,
 RA Tuddenham E.G.D., McVey J.H.;
 RT "Comparative sequence analysis and molecular evolution of blood
 coagulation genes from Gallus gallus and Fugu rubripes.";
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF465272; AA033367.1;
 DR GO; GO:0005507; F:coppper ion binding; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR001117; Cu-oxidase.
 DR InterPro; IPR008972; Cupredoxin.
 DR InterPro; IPR000421; FA58 C.
 DR Pfam; PF00394; Cu-oxidase; 1.
 DR PROSITE; PS01285; FA58C_1; 2.
 DR PROSITE; PS01286; FA58C_2; 2.
 DR PROSITE; PS00022; FA58C_3; 2.
 DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; 2.
 FT NON TER 1
 SQ SEQUENCE 1377 AA; 152728 MW; 15ACFD7F7656565CD CRC64;

Query Match 65.2%; Score 568; DB 13; Length 1377;
 Best Local Similarity 61.0%; Pred. No. 3.3e-49;
 Matches 100; Conservative 30; Mismatches 34; Indels 0; Gaps 0;

QY 1 CDLNSCMPGLMESKASDAQITASSYFTNNFATWSPSKARHLQGRSNARWPOVNNPKE 60
 DB 1214 CDLNSCMPGLMESKIGIPDQIRASISSYNNFSSNSPQARLNLQGRINARWPTNSPSE 1273

QY 61 WLQVDFQKTMKVTGVTQGVKSLTSMYVKEFLISSQDGHQWTLFPQNGKVKVQFQNGD 120
 DB 1274 WLQVDFQKTMKVTGVTQGVKSLTSMYVKEFLISSQDGHQWTLFPQNGKVKVQFQNGD 1333

QY 121 SFTPVNSLDPELLTRYLRHQPQSWHQAIALRMEVLGCEAQLD 164
 DB 1334 YTSIVNSLSEPLFARYVRHPRWHNHIALRIEFLGCDTQOEY 1377

RESULT 6

Q804W6 PRELIMINARY; PRT; 1639 AA.
 ID Q804W6;
 AC Q804W6;
 DT 01-JUN-2003 (TRENBLrel. 24, Created)
 DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Coagulation factor VIII precursor.
 GN F8.
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neoceratopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Takifugu.
 OX NCBI_TaxID=31033;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Davidson C.J., Hirt R.P., Lal K., Snell P., Elgar G.,
 RA Tuddenham E.G.D., McVey J.H.;
 RT "Comparative sequence analysis and molecular evolution of blood
 coagulation genes from Gallus gallus and Fugu rubripes.";
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF465279; AA033374.1;
 DR GO; GO:0005507; F:coppper ion binding; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR001117; Cu-oxidase.
 DR InterPro; IPR008972; Cupredoxin.
 DR InterPro; IPR000421; FA58 C.
 DR InterPro; IPR008979; Gal Bind like.
 DR Pfam; PF00394; Cu-oxidase; 2.
 DR Pfam; PF00754; F5_F8 type_C; 2.
 DR SMART; SM00231; FA58C_2.
 DR PROSITE; PS01285; FA58C_1; 2.
 DR PROSITE; PS01286; FA58C_2; 2.
 DR PROSITE; PS00022; FA58C_3; 2.
 DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; 2.
 SQ SEQUENCE 1639 AA; 185203 MW; 881778AFFF09006 CRC64;

Query Match 53.4%; Score 465; DB 13; Length 1639;
 Best Local Similarity 50.9%; Pred. No. 1.6e-38;
 Matches 83; Conservative 28; Mismatches 50; Indels 2; Gaps 1;

QY 1 CDLNSCMPGLMESKASDAQITASSYFTNNFATWSPSKARHLQGRSNARWPOVNNPKE 60
 DB 1474 CDLNSCPLGLQDRRIPEDESFASSYSWLSRWPISLARLHQGSANARWPKNNPHE 1533

QY 61 WLQVDFQKTMKVTGVTQGVKSLTSMYVKEFLISSQDGHQWTLFPQNG--KVKVQFN 118
 DB 1534 WLQVDFQKTMKVTGVTQGVKSLTSMYVKEFLISSQDGHQWTLFPQNG--KVKVQFN 1593

QY 119 QDSFTPVNSLDPELLTRYLRHQPQSWHQAIALRMEVLGCEAQLD 161
 DB 1594 NDSDEALITFDAPLFGYRIHPLGWINDLALRLEVLGCDTQ 1636

RESULT 7

Q7SZNO PRELIMINARY; PRT; 1460 AA.
 ID Q7SZNO;
 AC Q7SZNO;
 DT 01-OCT-2003 (TRENBLrel. 25, Created)
 DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Pseutarin C precursor.
 GN Pseudonaja textilis (Eastern brown snake).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Acanthophiinae; Pseudonaja.
 OX NCBI_TaxID=8673;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RX MEDLINE=22781770; PubMed=12730119;
 Rao V.S., Swarup S., Kini R.M.;

DE Ac2-120.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Xu C.S., Li W.O., Li Y.C., Han H.P., Wang G.P., Chai L.Q., Yuan J.Y.,
 RA Yang K.J., Yan H.M., Chang C.F., Zhao L.F., Ma H., Wang L., Wang S.F.,
 RA Shi J.B., Rahman S., Wang Q.N., Zhang J.B.;
 RT "Liver regeneration after PH";
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY321333; AAP86265.1; -
 SQ SEQUENCE 2102 AA; 237257 MW; 001BCB7DE31AC560 CRC64;

Query Match 44.2%; Score 385; DB 11; Length 2102;
 Best Local Similarity 44.3%; Pred. No. 3.7e-30;
 Matches 74; Conservative 34; Mismatches 53; Indels 6; Gaps 3;

QY 1 CDLNSCSMPGLMESKASDAQITASSYFTNMFAT-WSPSKARLHLQGRSNARWPQVNP 59
 DB 1939 CEVNGCSTPLGLEDRIGNQKITASSFKKSWGSGYWEPSLARLNAQGRVNAWQAKANNK 1998

QY 60 EWLVDFQKMTKVTGVTQGVKSLTSMYKFLISSQDGHOWTLFFQNGKV--KVFOG 117
 DB 1999 QWLQDLKTKVTAIVTQCKLSSEMYVKSYSILYSDGVSKWFKYRKSSMVDKIFEG 2058

QY 118 NQDSFTPVNSLDPPLTRYLRHPQSWHQAIALRMEVLGCEAQDLY 164
 DB 2059 NSNTKGHKMKFFPPIISRIRIPIKTNQSIARLLELFGC---DIV 2102

RESULT 11
 QN610 PRELIMINARY; PRT; 480 AA.
 ID QN610;
 AC QN610;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE EGF-like repeats and discoidin I-like domains 3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC030828; AAH30828.1; -
 DR GO; GO:0005509; P:calcium ion binding; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR000152; Asx_hydroxyl_S.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR000421; FA58_C.
 DR InterPro; IPR008579; Gal_Bind_like.
 DR InterPro; IPR006210; IEGF.
 DR Pfam; PF00008; EGF; 3.
 DR Pfam; PF00754; F5_F8_type_C; 2.
 DR SMART; SM00181; EGF; 3.
 DR SMART; SM00179; EGF_Ca; 3.
 DR SMART; SM00231; FA58C; 2.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; 2.
 DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS01187; EGF_Ca; 1.
 DR PROSITE; PS01285; FA58C_1; 2.
 DR PROSITE; PS01286; FA58C_2; 2.
 DR PROSITE; PS00022; FA58C_3; 2.
 DR EGF-like domain.
 KW EGF-like domain.
 SQ SEQUENCE 480 AA; 53795 MW; 884B47ACFA507211 CRC64;

Query Match 42.1%; Score 366.5; DB 4; Length 480;
 Best Local Similarity 46.4%; Pred. No. 4.5e-29;
 Matches 78; Conservative 24; Mismatches 59; Indels 7; Gaps 3;

QY 1 CDLNSCSMPGLMESKASDAQITASSYF-----TNMFATWSPSKARLHLQGRSNARWPQV 56
 DB 314 CELSGCSEPLGMSKSGH:QDYQITASSIFRLNMDMF-TWEPKARLDKQKRVNWTSGHN 372

QY 57 NPKSWLQVDFQKMTKVTGVTQGVKSLTSMYKFLISSQDGHOWTLF--FQNGKV 114
 DB 373 DQSQWLQVLDLVPTKVTGVTGILITQGAQKDFGHQVGSYKLAYSNDGEHWTVTQDEKQDKV 432

QY 115 FQGNQDSFTPVNSLDPPLTRYLRHPQSWHQAIALRMEVLGCEAQD 162
 DB 433 FQGNFDNDTHRNKVIDPPIYARHRIILFWISWYGRITLRSLLGCTEEB 480

RESULT 12
 Q43854 PRELIMINARY; PRT; 480 AA.
 ID Q43854;
 AC Q43854; O43855;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Integrin-binding protein DEL1 precursor.
 GN DEL1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND CHARACTERIZATION.
 RC TISSUE=Embryonic lung;
 RX MEDLINE=98083109; PubMed=9420328;
 RA Hidai C., Zupancic T.J., Penta K., Mikhail A., Kawana M.,
 RA Quertemous E.E., Aoka Y., Fukagawa M., Matsui Y., Platika D.,
 RA Auerbach R., Hogan B.L.M., Snodgrass R., Quertemous T.;
 RT "Cloning and characterization of developmental endothelial locus-1: an
 RT embryonic endothelial cell protein that binds the alphavbeta3 integrin
 RT receptor.";
 RL Genes Dev. 12:121-33(1998).
 CC -!- FUNCTION: PROMOTES ADHESION OF ENDOTHELIAL CELLS THROUGH
 CC INTERACTION WITH THE ALPHA-V BETA3 INTEGRIN RECEPTOR. INHIBITS
 CC REGULATION OF VASCULAR-LIKE STRUCTURES. MAY BE INVOLVED IN
 CC DEVELOPMENT.
 CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=Long;
 CC IsoId=Q43854-1; Sequence=Displayed;
 CC Name=Short;
 CC IsoId=Q43854-2; Sequence=VSP_050006, VSP_050007;
 CC -!- SIMILARITY: CONTAINS 3 EGF-LIKE DOMAINS.
 CC -!- SIMILARITY: CONTAINS 2 F5/F8 TYPE C DOMAINS.
 DR EMBL; U70312; AAC02648.1; -
 DR EMBL; U70313; AAC02649.1; -
 DR HSSP; P12259; 1CZT.
 DR Genew; HGNC:3173; EDIL3.
 DR GO; GO:0005176; P:integrin binding; TAS.
 DR InterPro; IPR000152; Asx_hydroxyl_S.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR000421; FA58_C.
 DR InterPro; IPR008579; Gal_Bind_like.
 DR Pfam; PF00008; EGF; 3.
 DR Pfam; PF00754; F5_F8_type_C; 2.
 DR SMART; SM00179; EGF_Ca; 1.
 DR SMART; SM00231; FA58C; 2.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; 2.

```

DR PROSITE: PS01186; EGF 2; 2.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS01285; FA58C.1; 2.
DR PROSITE: PS01286; FA58C.2; 2.
DR PROSITE: PS00022; FA58C.3; 2.
KW EGF-like domain; Alternative splicing; Signal; Developmental protein;
KW Cell adhesion; Repeat.
FT SIGNAL 1 16
FT CHAIN 17 480
FT DOMAIN 26 59
FT DOMAIN 78 116
FT DOMAIN 123 154
FT DOMAIN 161 311
FT DOMAIN 322 473
FT SITE 96 98
FT DISULFID 26 37
FT DISULFID 31 48
FT DISULFID 50 59
FT DISULFID 78 89
FT DISULFID 83 105
FT DISULFID 107 116
FT DISULFID 158 314
FT DISULFID 301 305
FT DISULFID 319 476
FT VARSPPLIC 66 66
FT VARSPPLIC 67 76
FT FT FT
SQ SEQUENCE 480 AA; 53765 MW; P7171E2JA309FD48 CRC64;

Query Match 42.1%; Score 366.5; DB 4; Length 480;
Best Local Similarity 46.4%; Pred. No. 4.5e-29;
Matches 78; Conservative 24; Mismatches 59; Indels 7; Gaps 3;

QY 1 CDLNSCSMPGLMGESKAISDAQITASSYFTNMPA-TWSPSKARLHLQGRSNARPPQVNNPK 56
DQ 314 CELSGCSEPLGMEKGLIDDSKITASSVSNWYSGQWHPWYARLNKQGTANAWQAKNNDIQ 372
QY 57 NPKELQVDFQKTMKVTGTTQGVKSLTSMYKVEFLISSQDGHQWTLFPQNG--KVKVFOG 114
DQ 373 DQSQWLQVLLVPTKVTGTTQGVKSLTSMYKVEFLISSQDGHQWTLFPQNG--KVKVFOG 432
QY 115 FQGNQDSFTPVNSLDPLLRVLRHPQSWVHQIALRMEVLGCEA 162
DQ 433 FQGNFNDTHRKVNDPDPPIYARHILPWSWYGRITLRSELLGCTEE 480

RESULT 13
ID Q8AYEO PRELIMINARY; PRT; 407 AA.
AC Q8AYEO
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Coagulation factor V [Fragment].
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteiophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Hanumanthaiah R., Day K., Jagadeeswaran P.;
RT "Comprehensive analysis of blood coagulation pathways in teleostei:
RT Evolution of coagulation factor genes and identification of zebrafish
RT factor VIII.";
RL Blood Cells Mol. Dis. 0:0-0(2002).
DR EMBL; AF515275; AAN71005.1; -.
DR GO; GO:0005507; F:cell adhesion; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR001117; Cu-oxidase.
DR InterPro; IPR008972; Cupredoxin.
DR InterPro; IPR000421; FA58_C.
DR PROSITE; PS01285; FA58C.1; 2.
DR PROSITE; PS01286; FA58C.2; 1.
DR PROSITE; PS00022; FA58C.3; 2.
DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; 3.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Hanumanthaiah R., Day K., Jagadeeswaran P.;
RT "Comprehensive analysis of blood coagulation pathways in teleostei:
RT Evolution of coagulation factor genes and identification of zebrafish
RT factor VIII.";
RL Blood Cells Mol. Dis. 0:0-0(2002).
DR EMBL; AF515275; AAN71005.1; -.
DR GO; GO:0005507; F:cell adhesion; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR001117; Cu-oxidase.
DR InterPro; IPR008972; Cupredoxin.
DR InterPro; IPR000421; FA58_C.

```

```

DR InterPro; IPR008979; Gal_bind_like.
DR Pfam; PF00754; F5_F8_type_C; 2.
DR SMART; SM00231; FA58C; 2.
DR PROSITE; PS01285; FA58C.1; 2.
DR PROSITE; PS01286; FA58C.2; 1.
DR PROSITE; PS00022; FA58C.3; 2.
DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; 1.
FT NON_TER 1
FT CHAIN 1 166D7EC7B78E7894 CRC64;
SQ SEQUENCE 407 AA; 46690 MW; 166D7EC7B78E7894 CRC64;

Query Match 42.0%; Score 365.5; DB 13; Length 407;
Best Local Similarity 39.5%; Pred. No. 4.6e-29;
Matches 64; Conservative 45; Mismatches 50; Indels 3; Gaps 2;

QY 1 CDLNSCSMPGLMGESKAISDAQITASSYFTNMPA-TWSPSKARLHLQGRSNARPPQVNNPK 59
DQ 244 CELDGCSEPLGMEKGLIDDSKITASSVSNWYSGQWHPWYARLNKQGTANAWQAKNNDIQ 303
QY 60 EWLQVDFQKTMKVTGTTQGVKSLTSMYKVEFLISSQDGHQWTLFPQNG--KVKVFOG 117
DQ 304 PWIQVELKEVKITGIVTQGAQSGNEMFVRSYILEYSEDGRRWKKYTDGDDYEQKLFQ 363
QY 118 NQDSFTPVNSLDPLLRVLRHPQSWVHQIALRMEVLGCE 159
DQ 364 NTDNNGQIKNYIPFISRFIRIIPKQWQSVNRIELGCD 405

RESULT 14
ID Q90X47 PRELIMINARY; PRT; 2119 AA.
AC Q90X47
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE SC1BZ2015.3 (Novel protein similar to vertebrate coagulation factor V
DE and VIII).
GN SC1BZ2015.3.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteiophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Lloyd D.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
DR EMBL; AL590146; CAC94896.1; -.
DR GO; GO:0005507; F:cell adhesion; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR001117; Cu-oxidase.
DR InterPro; IPR008972; Cupredoxin.
DR InterPro; IPR000421; FA58_C.
DR InterPro; IPR008979; Gal_bind_like.
DR Pfam; PF00394; Cu-oxidase; 2.
DR Pfam; PF00754; F5_F8_type_C; 2.
DR SMART; SM00231; FA58C; 2.
DR PROSITE; PS01285; FA58C.1; 2.
DR PROSITE; PS01286; FA58C.2; 1.
DR PROSITE; PS00022; FA58C.3; 2.
DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; 3.
SQ SEQUENCE 2119 AA; 240643 MW; DCOE806FFA8761B6 CRC64;

Query Match 42.0%; Score 365.5; DB 13; Length 2119;
Best Local Similarity 39.5%; Pred. No. 3.8e-28;
Matches 64; Conservative 45; Mismatches 50; Indels 3; Gaps 2;

QY 1 CDLNSCSMPGLMGESKAISDAQITASSYFTNMPA-TWSPSKARLHLQGRSNARPPQVNNPK 59
DQ 1956 CELDGCSEPLGMEKGLIDDSKITASSVSNWYSGQWHPWYARLNKQGTANAWQAKNNDIQ 2015
QY 60 EWLQVDFQKTMKVTGTTQGVKSLTSMYKVEFLISSQDGHQWTLFPQNG--KVKVFOG 117

```


Db 2016 PWIQVELKEYKITGIVTQAKSGNMFVRSVILEYSEDGRWMKYTDDEQKLFQ 2075

Qy 118 NQJSPFPVNSLDPPLTRYLRHPSQSVHFQIALRMEVLGC 159

Db 2076 NTDNGGQIKNYIYPFIRFIRIPKQWQKSVTRIELJGCD 2117

RESULT 15

Q9WTS3 PRELIMINARY; PRT; 426 AA.

AC Q9WTS3, 1999 (TrEMBLrel. 12, Created)

DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Milk fat globule glycoprotein MFG-E8 S (Similar to milk fat globule-SGF factor 8 protein).

GN MFG-E8.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN (1)

RP SEQUENCE FROM N.A.

RC STRAIN=BALB/C; TISSUE=Mammary gland;

RX MEDLINE=99120894; PubMed=9920772;

RA Oshima K., Aoki N., Negi M., Kishii M., Kitajima K., Matsuoka T.,

RT "Lactation-dependent expression of an mRNA splice variant with an exon

RT for a multiply O-glycosylated domain of mouse milk fat globule

RT glycoprotein MFG-E8.";

RL Biochem. Biophys. Res. Commun. 254:522-528(1999).

RN (2)

RP SEQUENCE FROM N.A.

RA Strausberg R.;

RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

RN (3)

RP SEQUENCE FROM N.A.

RC STRAIN=NOD;

RX MEDLINE=22354683; PubMed=12466851;

RA The FANTOM Consortium,

RA the RIKEN Genome Exploration Research Group Phase I & II Team;

RT "Analysis of the mouse transcriptome based on functional annotation of

RT 60,770 full-length cDNAs.";

RL Nature 420:563-573(2002).

CC -1- SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.

DR EMBL; AB025280; BAA76386.1; -

DR EMBL; BC003904; AA03904.1; -

DR EMBL; BC003892; AA03892.1; -

DR EMBL; AK089211; BAC40794.1; -

DR HSSP; P00740; 1EDM.

DR MGD; MGI:102768; Mfge8.

DR GO; GO:0007155; P:Cell adhesion; IEA.

DR InterPro; IPR001438; EGF-II.

DR InterPro; IPR006209; EGF-like.

DR InterPro; IPR000421; FAS8_C.

DR InterPro; IPR008979; Gal_bind_like.

DR InterPro; IPR006210; IEGF.

DR Pfam; PF00008; EGF; 2.

DR Pfam; PF00754; F5_F8_type_C; 2.

DR PRINTS; PRO0010; EGFELOOD.

DR SMART; SM00181; EGF; 2.

DR SMART; SM00231; FAS8C; 2.

DR PROSITE; PS00022; EGF 1; 2.

DR PROSITE; PS01186; EGF 2; 2.

DR PROSITE; PS01285; FAS8C_1; 2.

DR PROSITE; PS01286; FAS8C_2; 2.

DR PROSITE; PS00022; FAS8C_3; 2.

EW EGF-like domain.

SQ SEQUENCE 426 AA; 47197 MW; B:82FAA20629881A CRC64;

Query Match 41.0%; Score 357.5; DB 11; Length 426;

Best Local Similarity 43.5%; Pred. No. 3.2e-28;

Matches 70; Conservative 31; Mismatches 57; Indels 3; Gaps 2;

Qy 1 CDLNSCSMPLGWSKASDAQITASSYPT--NMFA-TWSPSKARHLQGRNWRPQVNN 57

Db 266 CELHGCSEPLGLKNNITPDSQMSASSYKTNLRAFGWYPHLGRLDNQKINAWTAQNS 325

Qy 58 PKEWLQVDFQKTMKVTGTQGVKSLLTSMVYKEFLISSODGHQWTLFFONGKVKVFOG 117

Db 326 AKENLQVLDGTQRQVGTITQGDFFGHIQVYASYKVAHSDDGQVQWTVYEEGSGSKVFOG 385

Qy 118 NQDSFTPVVNSLDPPPLTRYLRHPSQSVHFQIALRMEVLGC 158

Db 386 NLDNNSHKKNIFEKPFMARYVRVLPVSWHNRITLRLELLGC 426

Search completed: September 29, 2004, 16:39:45

Job time : 43 secs

This Page Blank (uspto)

GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model
Run on: September 29, 2004, 16:35:58 ; Search time 15 seconds
(without alignments)
1051.694 Million cell updates/sec

Title: US-10-049-399A-1_COPY_2169_2332
Perfect score: 871
Sequence: 1 CDLNSCSMPLGMSKAISDA.....WVHQIALRMEVLGCEAQDLY 164

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	871	100.0	216	2 A44258	factor VIII-associ
2	871	100.0	2351	1 EZHU	coagulation factor
3	752	86.3	2319	2 A47004	coagulation factor
4	720	82.7	2133	2 T42763	coagulation factor
5	390	44.8	2183	2 T42764	coagulation factor
6	380	43.6	2224	1 KFHUS	coagulation factor
7	379	43.5	2211	1 KPBOS	coagulation factor
8	367.5	42.2	427	2 JC4915	ags protein precu
9	353.5	40.6	463	1 A36479	milk fat globule m
10	328.5	37.7	409	2 T11743	pp47 protein - pig
11	327.5	37.6	218	2 A47285	milk fat globule p
12	324.5	37.3	401	2 S65138	glycoprotein anti
13	324.5	37.3	427	2 S74211	PA5-6/7 protein pr
14	262	30.1	845	2 JC5256	adipocyte transcr
15	254.5	29.2	927	1 JQ0948	A5 antigen precu
16	234.5	26.9	3133	2 S52093	hemocytin - silkwo
17	221	25.4	719	2 S51739	transcription repr
18	207.5	23.8	737	2 T31349	hypothetical prote
19	206.5	23.7	737	2 T15615	hypothetical prote
20	193	22.2	913	2 A48280	receptor tyrosine
21	192	22.0	876	2 A49508	protein-tyrosine k
22	184	21.1	1283	2 T13799	neurexin IV - frul
23	183	21.0	910	2 A53137	tyrosine kinase re
24	176.5	20.3	855	2 S42621	protein-tyrosine k
25	171	19.6	1381	2 T31083	paranodin - rat
26	171	19.6	1385	2 T41458	neurexin IV - mous
27	156.5	18.0	819	2 I48859	tyro 10 receptor k
28	134.5	15.4	791	2 T16031	hypothetical prote
29	84.5	9.7	149	1 DLD01D	discooidin I chain

30 84.5 9.7 149 2 B03382 discooidin I chain
31 84.5 9.7 253 1 DLD01C discooidin I chain
32 82.5 9.5 253 1 DLD01A discooidin I chain
33 80.5 9.2 157 2 H69849 hypothetical prote
34 80.5 9.2 881 2 S67026 probable membrane
35 79 9.1 334 2 H75362 hypothetical prote
36 79 9.1 464 2 T01324 hypothetical prote
37 78.5 9.0 762 2 H71916 DNA mismatch repai
38 78 9.0 491 2 I40455 penicillin binding
39 78 9.0 1134 2 T20332 hypothetical prote
40 77.5 8.9 1828 2 B59254 myosin heavy chain
41 77.5 8.9 1853 1 A46761 myosin heavy chain
42 77.5 8.9 1855 2 A59254 myosin heavy chain
43 76 8.7 202 2 AC0168 probable outer-mem
44 76 8.7 551 2 C64894 hypothetical prote
45 75 8.6 589 2 T35784 probable secreted

ALIGNMENTS

RESULT 1
A44258
factor VIII-associated gene B hypothetical protein - human
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 18-Jun-1999
C:Accession: A44258
R:Levinson, B.; Kenrick, S.; Gamel, P.; Fisher, K.; Gitschier, J.
Genomics 14, 585-589, 1992
A:Title: Evidence for a third transcript from the human factor VIII gene.
A:Reference number: A44258; MUID:93052386; PMID:1427887
A:Accession: A44258
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-216 <LEV>
A:Cross-references: GB:M90707; NID:G182316; PIDN:AAA58466.1; PID:G182317
C:Superfamily: coagulation factor VIII; discooidin I amino-terminal homology; ferroxiidas
F1-55/Domain: discooidin I amino-terminal homology #status atypical <DN1>
F:57-210/Domain: discooidin I amino-terminal homology <DN2>

Query Match 100.0%; Score 871; DB 2; Length 216;
Best Local Similarity 100.0%; Pred. No.:1.3e-76;
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CDLNSCSMPLGMSKAISDAQITASSYFTNNMFATWSPSKARLHLQGRSNAPRQVNNPKE 60
DB 53 CDLNSCSMPLGMSKAISDAQITASSYFTNNMFATWSPSKARLHLQGRSNAPRQVNNPKE 112
QY 61 WLQVDFQKTMKVTGVTTOGVKSLLTSMYVKBFLISSQDGHQWTLFFQNGKVKVFGNQD 120
DB 113 WLQVDFQKTMKVTGVTTOGVKSLLTSMYVKBFLISSQDGHQWTLFFQNGKVKVFGNQD 172
QY 121 STTPVNSLDPPLLTRYLRIRHPQSWVHOIALRMEVLGCEAQDLY 164
DB 173 STTPVNSLDPPLLTRYLRIRHPQSWVHOIALRMEVLGCEAQDLY 216

RESULT 2
EZHU
coagulation factor VIII precursor [validated] - human
N:Alternate names: antihemophilic factor A; coagulation factor VIIIc; procoagulant comp
C:Species: Homo sapiens (man)
C:Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 08-Dec-2000
C:Accession: I54318; A00525; I58059; A23584; A26174; A42348; A43986; S66445; B4
R:Gitschier, J.; Wood, W.I.
Hum. Mol. Genet. 1, 199-200, 1992
A:Title: Sequence of the exon-containing regions of the human factor VIII gene.
A:Reference number: I54318; MUID:93265012; PMID:1303178
A:Accession: I54318
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1921, 'S', 1923-2351 <RES>
A:Cross-references: GB:M88648; NID:G182381; PIDN:AAA52420.1; PID:G182383

R;Wood, W.I.; Capon, D.J.; Simonsen, C.C.; Eaton, D.L.; Gitschier, J.; Keyt, B.; Seeburg Nature 312, 330-337, 1984
 A>Title: Expression of active human factor VIII from recombinant DNA clones.
 A;Reference number: A00525; MUID:85061548; PMID:6438526
 A;Accession: A00525
 A;Molecule type: mRNA
 A;Residues: 1-2351 <MOO>
 A;Cross-references: EMBL:X01165; EMBL:X01166; EMBL:X01179
 R;Toole, J.J.; Knopf, J.B.; Wozney, J.M.; Sultzman, L.A.; Pittman, D.D.; S, D.N.; Hewick, R.M.
 Nature 312, 342-347, 1984
 A>Title: Molecular cloning of a cDNA encoding human antihemophilic factor.
 A;Reference number: I58059; MUID:85061550; PMID:6438528
 A;Accession: I58059
 A;Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-74, 'V', 76-1259, 'E', 1261-2351 <RE2>
 A;Cross-references: GB:X01740; NID:G182802; PIDN:AAA52484.1; PID:G182803
 R;Truett, M.A.; Blacher, R.; Burke, R.L.; Caput, D.; Chu, C.; Dina, D.; Hartog, K.; Kuo, B.; Randolph, A.; Urdea, M.S.; Valenzuela, P.; Dahl, H.H.; Favalaro, J.; Hansen, J.; N DNA 4, 333-349, 1985
 A>Title: Characterization of the polypeptide composition of human factor VIII:C and the
 A;Reference number: A23584; MUID:86081164; PMID:3935400
 A;Accession: A23584
 A;Molecule type: mRNA
 A;Residues: 1-2351 <TRU>
 A;Cross-references: GB:M14113; NID:G182817; PIDN:AAA52485.1; PID:G182818
 R;Eaton, D.; Rodriguez, H.; Vehar, G.A.
 Biochemistry 25, 505-512, 1986
 A>Title: Proteolytic processing of human factor VIII. Correlation of specific cleavages
 ity.
 A;Reference number: A26174; MUID:86159740; PMID:3082357
 A;Accession: A26174
 A;Molecule type: protein
 A;Residues: 20-36;392-399, 'X', 401-402;1668-1678;1709-1722, 'D', 1723-1725;1741-1755 <EAT>
 R;Pittman, D.D.; Wang, J.H.; Kaufman, R.J.
 Biochemistry 31, 3315-3325, 1992
 A>Title: Identification and functional importance of tyrosine sulfate residues within re
 A;Reference number: A42348; MUID:92207952; PMID:1554716
 A;Accession: A42348
 A;Molecule type: protein
 A;Residues: 20-36;356-371;392-408;582-594;1668-1669, 'X', 1671;1672-1692;1693-1708;1709-17
 A;Experimental source: recombinant material from Chinese hamster ovary cells
 A;Note: sequence extracted from NCBI backbone and corrected to correspond with the publi
 R;Pay, P.J.; Smudzin, T.M.
 J. Biol. Chem. 264, 14005-14010, 1989
 A>Title: Intersubunit fluorescence energy transfer in human factor VIII.
 A;Reference number: A43986; MUID:89340500; PMID:2503509
 A;Accession: A43986
 A;Molecule type: protein
 A;Residues: 'X', 517-523;1853-1860, 'X', 1862-1864, 'X', 1866 <PAY>
 R;Leyte, A.; van Schijndel, H.B.; Niehrs, C.; Huttner, W.B.; Verbeet, M.P.; Mertens, K.; J. Biol. Chem. 266, 740-746, 1991
 A>Title: Sulfation of Tyr(1680) of human blood coagulation factor VIII is essential for
 A;Reference number: A56109; MUID:91093266; PMID:1898735
 A;Accession: A56109
 A;Contents: annotation; sulfation
 R;Gitschier, J.; Wood, W.I.; Goralka, T.M.; Wilson, K.L.; Chen, E.Y.; Eaton, D.H.; Vehar, Nature 312, 326-330, 1984
 A>Title: Characterization of the human factor VIII gene.
 A;Reference number: A56196; MUID:85061547; PMID:6438525
 A;Contents: annotation; introns
 R;McMullen, B.A.; Fujikawa, K.; Davie, E.W.; Hedner, U.; Ezban, M.
 Protein Sci. 4, 740-746, 1995
 A>Title: Locations of disulfide bonds and free cysteines in the heavy and light chains o
 A;Reference number: A5216; MUID:95338127; PMID:7613471
 A;Contents: annotation; disulfide bonds
 R;Kjalke, M.; Heding, A.; Talbo, G.; Persson, E.; Thomsen, J.; Ezban, M.
 Eur. J. Biochem. 234, 773-779, 1995
 A>Title: Amino acid residues 721-729 are required for full factor VIII activity.
 A;Reference number: S63527; MUID:96163459; PMID:8575434
 A;Accession: S63527
 A;Molecule type: protein

A;Residues: 733-752;753-759 <XJA>
 R;Lind, P.; Larsson, K.; Spira, J.; Sydow-Baeckman, M.; Almstedt, A.; Gray, E.; Sandberg Eur. J. Biochem. 232, 19-27, 1995
 A>Title: Novel forms of B-domain-deleted recombinant factor VIII molecules. Construction
 A;Reference number: S66445; MUID:96048024; PMID:7556150
 A;Accession: S66445
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1669-1685 <LIN>
 C;Comment: Factor VIII is activated by factor Xa and thrombin, but prolonged exposure pr
 C;Genetics:
 A;Gene: GDB:F8C
 A;Cross-references: GDB:119124; OMIM:306700
 A;Map position: Xq28-Xq28
 A;Introns: 48/2; 89/1; 130/1; 201/1; 224/1; 263/1; 337/1; 424/2; 481/3; 513/1; 584/3; 63
 C;Function:
 A;Description: acts as a cofactor, with calcium and phospholipid, for the factor IXa pro
 A;Pathway: blood coagulation
 C;Superfamily: coagulation factor VIII; disocidin I amino-terminal homology; ferroxidase
 C;Keywords: acute phase; blood coagulation; duplication; glycoprotein; hemophilia A; pla
 F;1-19/Domain: signal sequence #status predicted <Sig>
 F;20-2351/Product: coagulation factor VIII #status experimental <MAT>
 F;20-740/Product: coagulation factor VIIa heavy chain #status experimental <ACH>
 F;20-356/Domain: A1 <DA1>
 F;23-348/Domain: ferroxidase repeat homology <FO1>
 F;392-759/Domain: A2 <DA2>
 F;402-730/Domain: ferroxidase repeat homology <FO2>
 F;760-1667/Domain: B <DB0>
 F;1668-2351/Product: coagulation factor VIIa light chain #status experimental <ACL>
 F;1709-2038/Domain: A3 <DA3>
 F;1716-2038/Domain: ferroxidase repeat homology <FO3>
 F;2039-2191/Domain: C1 <DC1>
 F;2039-2188/Domain: disocidin I amino-terminal homology <DN1>
 F;2132-2351/Domain: C2 <DC2>
 F;2132-2345/Domain: disocidin I amino-terminal homology <DN2>
 F;602-258, 601, 776, 803, 847, 919, 962, 1020, 1024, 1074, 1085, 1204, 1274, 1278, 1301, 1319, 1403, 1
 F;172-198, 267-348, 547-573, 649-730, 1851-1877, 1918-1922, 2040-2188/Disulfide bonds: #status
 F;355-356/Cleavage site: Arg-Met (coagulation factor Xa, protein C) #status predicted
 F;365, 737, 738, 742, 1683, 1699/Binding site: sulfate (Tyr) (covalent) #status experimental
 F;391-392/Cleavage site: Arg-Ser (coagulation factor Xa, thrombin) #status experimental
 F;414, 426/Binding site: sulfate (Tyr) (covalent) #status predicted
 F;759-760/Cleavage site: Arg-Ser (coagulation factor Xa, thrombin) #status experimental
 F;1667-1668/Cleavage site: Arg-Glu (unidentified proteinase) #status experimental
 F;1708-1709/Cleavage site: Arg-Ser (coagulation factor Xa, thrombin) #status experimental
 F;1740-1741/Cleavage site: Arg-Ala (coagulation factor Xa) #status experimental
 F;2193-2345/Disulfide bonds: #status predicted
 Query Match 100.0%; Score 871; DB 1; Length 2351;
 Best Local Similarity 100.0%; Pred. No. 2.6e-75;
 Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CDLNSCMP;LGMSKSAISDAQITASSYFTNMPATWSPSKARLHLOGRSNARPOVNNPK 60
 Db 2188 CDLNSCMP;LGMSKSAISDAQITASSYFTNMPATWSPSKARLHLOGRSNARPOVNNPK 2247
 Qy 61 WLQVDFOKTKVTVTGVTQGVKSLTSMYKFLISSSQDQHWTLPFQNGKVKVFGNQD 120
 Db 2248 WLQVDFOKTKVTVTGVTQGVKSLTSMYKFLISSSQDQHWTLPFQNGKVKVFGNQD 2307
 Qy 121 SFTPVNSLDPPLLTRYLRTHPSQSWHQAIRMEVLGCEAQDLY 164
 Db 2308 SFTPVNSLDPPLLTRYLRTHPSQSWHQAIRMEVLGCEAQDLY 2351
 RESULT 3
 A47004
 coagulation factor VIII precursor - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 18-Jun-1999
 C;Accession: A47004
 R;Eider, B.; Lakiach, D.; Gitschier, J.
 Genomics 16, 374-379, 1993
 A>Title: Sequence of the murine factor VIII cDNA.

A:Reference number: A47004; MUID:93300511; PMID:8314577
A:Accession: A47004
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-2319 <ELD>
A:Cross-references: GB:L05573; NID:g192456; PIDN:AAA37385.1; PID:g192457
C:Superfamily: coagulation factor VIII; discoicidin I amino-terminal homology; ferroxidase
F:1-19/Domain: signal sequence #status predicted <SIG>
F:19-349/Domain: ferroxidase repeat homology <FO2>
F:402-730/Domain: ferroxidase repeat homology <FO2>
F:1686-2006/Domain: ferroxidase repeat homology <FO3>
F:2007-2156/Domain: discoicidin I amino-terminal homology <DN1>
F:2160-2313/Domain: discoicidin I amino-terminal homology <DN2>

Query Match 86.3%; Score 752; DB 2; Length 2319;
Best Local Similarity 84.1%; Pred. No. 7.7e-64;
Matches 138; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 CDLNSCSMPGLGMSKAISSDAQITASSYFTNMFATWSPSKARLHLQGRSNARPPQVNNPK 60
Db 2156 CDLNSCSIPGLGMSKVISDTQITASSYFTNMFATWSPSKARLHLQGRTNARPPQVNDPKQ 2215

QY 61 WLQVDFQKTMKVTGVTQGVKSLTSMYKFEFLISSQDGHQWTLFPQNGKVKVFGQND 120
Db 2216 WLQVDFQKTMKVTGVTQGVKSLTSMYKFEFLISSQDGHQWTLFPQNGKVKVFGQND 2275

QY 121 SFTPVNSLDPLLTRYLRIHPQSWVHQIALRMEVLGCEAQDLY 164
Db 2276 SSTPMNSLDPLLTRYLRIHPQSWVHQIALRMEVLGCEAQDLY 2319

RESULT 4
T42763
coagulation factor VIII precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jun-2000
C:Accession: T42763
R:Lollar, P.
Submitted to the EMBL Data Library, August 1996
A:Reference number: Z22269
A:Accession: T42763
A:Molecule type: mRNA
A:Residues: 1-2133 <LOL>
A:Cross-references: EMBL:U94517; NID:g1511633; PID:g1511634; PIDN:AAB06705.1
C:Superfamily: coagulation factor VIII; discoicidin I amino-terminal homology; ferroxidase
C:Keywords: acute phase; blood coagulation; duplication; glycoprotein; hemophilia A; pla
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-2133/Product: coagulation factor VIII #status predicted <YAT>
F:23-349/Domain: ferroxidase repeat homology <FOX1>
F:402-730/Domain: ferroxidase repeat homology <FOX2>
F:1498-1820/Domain: ferroxidase repeat homology <FOX3>

Query Match 82.7%; Score 720; DB 2; Length 2133;
Best Local Similarity 79.9%; Pred. No. 8.5e-61;
Matches 131; Conservative 20; Mismatches 13; Indels 0; Gaps 0;

QY 1 CDLNSCSMPGLGMSKAISSDAQITASSYFTNMFATWSPSKARLHLQGRSNARPPQVNNPK 60
Db 1970 CDLNSCSMPGLGMSKAISSDAQITASSYFTNMFATWSPSKARLHLQGRTNARPPVSSAE 2029

QY 61 WLQVDFQKTMKVTGVTQGVKSLTSMYKFEFLISSQDGHQWTLFPQNGKVKVFGQND 120
Db 2030 WLQVDFQKTMKVTGVTQGVKSLTSMYKFEFLISSQDGHQWTLFPQNGKVKVFGQND 2089

QY 121 SFTPVNSLDPLLTRYLRIHPQSWVHQIALRMEVLGCEAQDLY 164
Db 2090 SSTPMNSLDPLLTRYLRIHPQSWVHQIALRMEVLGCEAQDLY 2133

RESULT 5
T42764
coagulation factor V - mouse

C:Species: Mus musculus (house mouse)
C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jun-2000
C:Accession: T42764
R:Yang, T.L.; Cui, J.; Rehmtulla, A.; Yang, A.; Mousalli, M.; Kaufman, R.J.; Ginsburg
Blood 91, 4593-4599, 1998
A:Title: The structure and function of murine factor V and its inactivation by protein
A:Reference number: Z22270; MUID:9828202; PMID:9616155
A:Accession: T42764
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-2183 <YAN>
A:Cross-references: EMBL:U52925; NID:g3219690; PID:g3219691; PIDN:AAC99553.1
C:Function:
A:Pathway: blood coagulation
C:Superfamily: coagulation factor V; discoicidin I amino-terminal homology; ferroxidase
C:Keywords: blood coagulation; duplication; glycoprotein; phospholipid binding; plasma;
F:1541-1864/Domain: ferroxidase repeat homology <FOX2>

Query Match 44.8%; Score 390; DB 2; Length 2183;
Best Local Similarity 45.5%; Pred. No. 6.1e-29;
Matches 76; Conservative 31; Mismatches 54; Indels 6; Gaps 3;

QY 1 CDLNSCSMPGLGMSKAISSDAQITASSYFTNMFATWSPSKARLHLQGRSNARPPQVNNPK 59
Db 2020 CEVAGCSTPLGLEDRIQDQKITASSSPKSKWGWYWEPSLARLNAQGRVNAWQAKANNK 2079

QY 60 EWLQVDFQKTMKVTGVTQGVKSLTSMYKFEFLISSQDGHQWTLFPQNGKVKVFGQND 117
Db 2080 QWLQVDFQKTMKVTGVTQGVKSLTSMYKFEFLISSQDGHQWTLFPQNGKVKVFGQND 2139

QY 118 NODSFTPVNSLDPLLTRYLRIHPQSWVHQIALRMEVLGCEAQDLY 164
Db 2140 NSNTKGHMFNFNPPIISRFIRIIPKTNQSIARLELFGC---DIY 2183

RESULT 6
KPHUS
coagulation factor V precursor [validated] - human
N:Alternate names: coagulation labile factor; proaccelerin
C:Species: Homo sapiens (man)
C>Date: 19-May-1989 #sequence_revision 02-Jun-1995 #text_change 08-Dec-2000
C:Accession: A56172; A42344; A28028; A27498; A25897
R:Cripe, L.D.; Moore, K.D.; Kane, W.H.
Biochemistry 31, 3777-3785, 1992
A:Title: Structure of the gene for human coagulation factor V.
A:Reference number: A42344; MUID:92232668; PMID:1567832
A:Accession: A56172
A:Molecule type: DNA
A:Residues: 1-2224 <CEI>
A:Cross-references: GB:J05368
A:Accession: A42344
A:Molecule type: DNA
A:Residues: 48-58; 79-89; 120-130; 191-201; 239-249; 313-323; 368-378; 428-437; 461-471; 533-542
2070; 2111-2120; 2172-2181 <CR2>
R:Jenny, R.J.; Pittman, D.D.; Toole, J.J.; Kriz, R.W.; Aldape, R.A.; Hewick, R.M.; Kauf
proc. Natl. Acad. Sci. U.S.A. 84, 4846-4850, 1987
A:Title: Complete cDNA and derived amino acid sequence of human factor V.
A:Reference number: A28028; MUID:87260886; PMID:3110773
A:Accession: A28028
A:Molecule type: mRNA
A:Residues: 1-857; 'R', 859-864; 'R', 866-924; 'E', 926-1763; 'I', 1765-2212; 'T', 2214-2224 <JEN
A:Cross-references: GB:M16967
A:Notes: parts of this sequence, including the amino end of the mature protein, were det
R:Kane, W.H.; Ichinose, A.; Hagen, F.S.; Davie, E.W.
Biochemistry 26, 6508-6514, 1987
A:Title: Cloning of cDNAs coding for the heavy chain region and connecting region of hu
A:Reference number: A27498; MUID:88107560; PMID:2827731
A:Accession: A27498
A:Molecule type: mRNA
A:Residues: 1-1284; 'I', 1286-1600 <KAN>
A:Cross-references: GB:M17785
A:Note: parts of this sequence were determined by protein sequencing

R:Kane, W.H.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 83, 6800-6804, 1986
 A:Title: Cloning of a cDNA coding for human factor V, a blood coagulation factor homolog
 A:Reference number: A25897; MUID:86513665; PMID:3092220
 A:Accession: A25897
 A:Molecule type: mRNA
 A:Residues: 1188-1215, 1315-2224 <KA2>
 A:Cross-references: GB:M14335
 A:Note: Parts of this sequence were determined by protein sequencing
 R:Keller, F.G.; Ortel, T.L.; Quinn-Alten, M.A.; Kane, W.H.
 Biochemistry 34, 4118-4124, 1995
 A:Title: Thrombin-catalyzed activation of recombinant human factor V.
 A:Reference number: A56139; MUID:95210278; PMID:7696276
 A:Contents: annotation; thrombin cleavage sites
 C:Comment: Factor V is activated by thrombin and partially by coagulation factor Xa.
 C:Genetics:
 A:Gene: GDB:F5
 A:Cross-references: GDB:119896; OMIM:227400
 A:Map position: 1q23-1q23
 A:Introns: 53/2; 84/1; 125/1; 196/1; 244/1; 318/1; 373/2; 432/3; 466/1; 537/3; 588/1; 65
 C:Function:
 A:Description: acts as a cofactor, with calcium and phospholipid, for the factor Xa pro
 A:Pathway: blood coagulation
 C:Superfamily: coagulation factor V; discoidin I amino-terminal homology; ferroxidase re
 C:Keywords: blood coagulation; duplication; glycoprotein; phospholipid binding; plasma;
 F:1-28/Domain: signal sequence #status predicted <SIG>
 F:28-2224/Product: coagulation factor V #status predicted <VAT>
 F:29-737/Product: coagulation factor Va heavy chain #status experimental <VAH>
 F:29-345/Domain: A1 <DA1>
 F:33-329/Domain: ferroxidase repeat homology <FO1>
 F:346-691/Domain: A2 <DA2>
 F:351-684/Domain: ferroxidase repeat homology <FO2>
 F:652-1573/Domain: B <DOB>
 F:1183-1461/Region: 9-residue repeats (Q-X-T-N-L-S-P-D-L-S)
 F:1574-2224/Product: coagulation factor Va light chain #status experimental <VAL>
 F:1581-1905/Domain: A3 <DA3>
 F:1581-1905/Domain: ferroxidase repeat homology <FO3>
 F:1667-1765/Region: phospholipid binding #status predicted
 F:1906-2064/Domain: C1 <DC1>
 F:1906-2061/Domain: discoidin I amino-terminal homology <DN1>
 F:2065-2224/Domain: C2 <DC2>
 F:2065-2221/Domain: discoidin I amino-terminal homology <DN2>
 F:51-55,239,297,460,468,554,741,752,760,776,782,821,938,977,1074,1083,1103,1106,1479,149
 F:167-193,248-329,460,553,587,745,756,774,780,902,952,964,1044,1053,1062,1071,1078,1094,
 F:334-335/Cleavage site: Arg-Asn (protein C) #status predicted
 F:363,697,1537/Binding site: Arg-Ser (coagulation factor Xa) #status predicted
 F:363,693,1546/Binding site: Arg-Ser (coagulation factor Xa) #status predicted
 F:376-377/Cleavage site: Arg-Ser (coagulation factor Xa) #status predicted
 F:382,1338/Binding site: carbohydrate (Asn) (covalent) #status absent
 F:534-535/Cleavage site: Arg-Gly (protein C) #status predicted
 F:737-738/Cleavage site: Arg-Thr (coagulation factor Xa, thrombin) #status experimental
 F:1046-1047/Cleavage site: Arg-Thr (coagulation factor Xa, thrombin) #status experimental
 F:1573-1574/Cleavage site: Arg-Ser (thrombin) #status experimental

Query Match 43.5%; Score 380; DB 1; Length 2224;
 Best Local Similarity 42.5%; Pred. No. 5.7e-28;
 Matches 71; Conservative 38; Mismatches 52; Indels 6; Gaps 3;

QY 1 CDLNSCMPLGESKAISSAQAITSYFFNMFAT-WSPSKARLHLQGRNAPQVNNPK 59
 Db 2061 CEVNGCSTPLGMEGSKIEKQITASSFKKSWGNYWEPFLARLNAGQGRVNAQKANNK 2120
 QY 60 EWLQVDFQTKMKTGVTGQVKSLLTSMYVKEFLISSODGHWTLFFQNGKV--KVFQ 117
 Db 2121 QMLEIDLLKIKITAITQCKSLSSSEMYVKSYYTHYSEQGVKPYRLKSWDKIFEG 2180
 QY 118 NQDSFTPVNSLDPPLLYRIHQSWHQTALRMEVLGCEAQDLY 164
 Db 2181 NNTKGHKNFNPPIISIRFIRVPTKNTQNSIALRLELFGC---DIY 2224

RESULT 7
 KFB05
 coagulation factor V precursor - bovine

C:Species: Bos primigenius taurus (cattle)
 C:Date: 04-Mar-1993 #sequence_revision 28-Apr-1995 #text_change 11-Jun-1999
 C:Accession: A42580; A36497
 R:Guinto, E.R.; Emon, C.T.; Mann, K.G.; MacGillivray, R.T.
 J. Biol. Chem. 267, 2971-2978, 1992
 A:Title: The complete cDNA sequence of bovine coagulation factor V.
 A:Reference number: A42580; MUID:92147638; PMID:1737753
 A:Accession: A42580
 A:Molecule type: mRNA
 A:Residues: 1-2211 <GU>
 A:Cross-references: GB:M81440; NID:G163037; PIDN:AAA30512.1; PID:G163038
 R:Kalafatis, M.; Jenny, R.J.; Mann, K.G.
 J. Biol. Chem. 265, 21580-21589, 1990
 A:Title: Identification and characterization of a phospholipid-binding site of bovine fa
 A:Reference number: A36497; MUID:91072354; PMID:2254316
 A:Accession: A36497
 A:Molecule type: protein
 A:Residues: 1566-1570, 'X', 1572-1581, 'X', 1583-1584; 1673-1676, 'X', 1678-1679, 'X', 1681, 'X', 1
 R:Xue, J.; Kalafatis, M.; Silveira, J.R.; Kung, C.; Mann, K.G.
 Biochemistry 33, 13109-13116, 1994
 A:Title: Determination of the disulfide bridges in factor Va heavy chain.
 A:Reference number: A55979; MUID:95034740; PMID:7947716
 A:Contents: annotation
 A:Note: 566-Cys and 617-Cys were shown to have free sulfhydryls
 C:Comment: Factor V is activated by thrombin and partially by coagulation factor Xa.
 C:Function:
 A:Description: acts as a cofactor, with calcium and phospholipid, for the factor Xa pro
 A:Pathway: blood coagulation
 C:Superfamily: coagulation factor V; discoidin I amino-terminal homology; ferroxidase re
 C:Keywords: blood coagulation; duplication; glycoprotein; phospholipid binding; plasma;
 F:1-28/Domain: signal sequence #status predicted <SIG>
 F:29-721/Product: coagulation factor V #status predicted <VAT>
 F:29-345/Domain: A1 <DA1>
 F:33-329/Domain: ferroxidase repeat homology <FO1>
 F:346-695/Domain: A2 <DA2>
 F:351-688/Domain: ferroxidase repeat homology <FO2>
 F:696-1564/Domain: B <DOB>
 F:1175-1437/Region: 9-residue repeats (Q-X-T-N-L-S-P-D-L-S)
 F:1565-1892/Domain: A3 <DA3>
 F:1572-1892/Domain: ferroxidase repeat homology <FO3>
 F:1654-1752/Region: phospholipid binding #status predicted
 F:1893-2051/Domain: C1 <DC1>
 F:1893-2048/Domain: discoidin I amino-terminal homology <DN1>
 F:2052-2211/Domain: C2 <DC2>
 F:2052-2208/Domain: discoidin I amino-terminal homology <DN2>
 F:167-193,248-329,499-525/Disulfide bonds: #status experimental
 F:225,239,297,382,460,553,587,745,756,774,780,902,952,964,1044,1053,1062,1071,1078,1094,
 F:334-335/Cleavage site: Arg-Asn (protein C) #status predicted
 F:363,697,1537/Binding site: Arg-Ser (coagulation factor Xa) #status predicted
 F:376-377/Cleavage site: Arg-Ser (coagulation factor Xa) #status predicted
 F:533-534/Cleavage site: Arg-Gly (protein C) #status predicted
 F:607-688,1712-1738,1894-2048,2053-2208/Disulfide bonds: #status predicted
 F:741-742/Cleavage site: Arg-Ser (coagulation factor Xa, thrombin) #status predicted
 F:1034-1035/Cleavage site: Arg-Ser (coagulation factor Xa, thrombin) #status predicted
 F:1564-1565/Cleavage site: Arg-Ser (thrombin) #status experimental

Query Match 43.5%; Score 379; DB 1; Length 2211;
 Best Local Similarity 43.7%; Pred. No. 7.1e-28;
 Matches 73; Conservative 32; Mismatches 56; Indels 6; Gaps 3;

QY 1 CDLNSCMPLGESKAISSAQAITSYFFNMFAT-WSPSKARLHLQGRNAPQVNNPK 59
 Db 2048 CEVNGCSTPLGMEGSKIEKQITASSFKKSWGNYWEPFLARLNAGQGRVNAQKANNK 2107
 QY 60 EWLQVDFQTKMKTGVTGQVKSLLTSMYVKEFLISSODGHWTLFFQNGKV--KVFQ 117
 Db 2108 QMLEIDLLKIKITAITQCKSLSSSEMYVKSYYTHYSEQGVKPYRLKSWDKIFEG 2167
 QY 118 NQDSFTPVNSLDPPLLYRIHQSWHQTALRMEVLGCEAQDLY 164

Db 2168 NNNVRGHVQNFNPPIISPIRIIPKWTNQSIARLRLLEFG---DMY 2211

RESULT 8
JC4915
ags protein precursor - rat
N:Alternate names: O-acetyl-Gd3 ganglioside
C:Species: Rattus norvegicus (Norway rat)
C:Date: 26-Sep-1996 #sequence_revision 01-Nov-1996 #text_change 20-Jun-2000
C:Accession: JC4915
R:Ogura, K.; Nara, K.; Watanabe, Y.; Kohno, K.; Tai, T.; Sanai, Y.
Biochem. Biophys. Res. Commun. 225, 932-938, 1996
A:Title: Cloning and expression of cDNA for O-acetylation of GD3 ganglioside.
A:Reference number: JC4915; MUID:96374422; PMID:8780713
A:Accession: JC4915
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-427 <OGU>
A:Cross-references: DDBJ:D84068; NID:gl620006; PIDN:BA12210.1; PID:gl620007
A:Experimental source: CST cell
C:Comment: This protein is required for the O-acetylation of disialoganglioside sialic acid.
A:Genetics:
C:Superfamily: milk fat globule protein; discoidin I amino-terminal homology; EGF homology
F:1-21/Domain: signal sequence #status predicted <SIG>
F:28-60/Domain: EGF homology <EG1>
F:68-107/Domain: EGF homology <EG2>
F:110-267/Domain: discoidin I amino-terminal homology <DN1>
F:271-427/Domain: discoidin I amino-terminal homology <DN2>

Query Match 42.2%; Score 367.5; DB 2; Length 427;
Best Local Similarity 45.3%; Pred. No. 1.2e-27;
Matches 73; Conservative 28; Mismatches 57; Indels 3; Gaps 2;

QY 1 CDLNSCMPUGMSKSAISDAQITASSYFT--NMFA-TWSPSKARLHLQGRSNWRQVYN 57
Db 267 CELHGGSEPLGLKNTIPDSQITASSSYKTWNLRFQWYFHLGLDNLQGNKINAWTAQSN 326
QY 58 PREWLQVDFQTKWKVTGVTQGVKSLTSMYVKEFLISSODGHQWTLFFQNGKVVFQ 117
Db 327 AKEWLQVDFQTKVTCITQGARDFGHIQVASYKVAHSDGQVTVVEEGTSTVFQ 386
QY 118 NQDSFTPVNLSPPPLTRYLRHPQSWHQAIALRMEVLGC 158
Db 387 NLDNNSHKKNIFEKPFPMARYVRVLPISWHNRITLRLELGC 427

RESULT 9
A36479
milk fat globule membrane protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A36479
R:Stubbs, J.D.; Lekutis, C.; Singer, K.L.; Bui, A.; Yuzuki, D.; Srinivasan, U.; Parry, G.
Proc. Natl. Acad. Sci. U.S.A. 87, 8417-8421, 1990
A:Title: cDNA cloning of a mouse mammary epithelial cell surface protein reveals the existence of a novel protein family.
A:Reference number: A36479; MUID:91046008; PMID:2122482
A:Accession: A36479
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-463 <STU>
A:Cross-references: DB:M38337; NID:gl99142; PIDN:AAA39534.1; PID:gi99143
C:Superfamily: milk fat globule protein; discoidin I amino-terminal homology; EGF homology
C:Keywords: membrane protein
F:28-60/Domain: EGF homology <EG1>
F:68-107/Domain: EGF homology <EG2>
F:147-303/Domain: discoidin I amino-terminal homology <DN1>
F:307-463/Domain: discoidin I amino-terminal homology <DN2>

Query Match 40.6%; Score 353.5; DB 1; Length 463;
Best Local Similarity 42.9%; Pred. No. 2.9e-26;
Matches 69; Conservative 32; Mismatches 57; Indels 3; Gaps 2;

Db 2168 NNNVRGHVQNFNPPIISPIRIIPKWTNQSIARLLEFG---DMY 2211

RESULT 8
JC4915
ags protein precursor - rat
N:Alternate names: O-acetyl-Gd3 ganglioside
C:Species: Rattus norvegicus (Norway rat)
C:Date: 26-Sep-1996 #sequence_revision 01-Nov-1996 #text_change 20-Jun-2000
C:Accession: JC4915
R:Ogura, K.; Nara, K.; Watanabe, Y.; Kohno, K.; Tai, T.; Sanai, Y.
Biochem. Biophys. Res. Commun. 225, 932-938, 1996
A:Title: Cloning and expression of cDNA for O-acetylation of GD3 ganglioside.
A:Reference number: JC4915; MUID:96374422; PMID:8780713
A:Accession: JC4915
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-427 <OGU>
A:Cross-references: DDBJ:D84068; NID:gl620006; PIDN:BA12210.1; PID:gl620007
A:Experimental source: CST cell
C:Comment: This protein is required for the O-acetylation of disialoganglioside sialic acid.
A:Genetics:
C:Superfamily: milk fat globule protein; discoidin I amino-terminal homology; EGF homology
F:1-21/Domain: signal sequence #status predicted <SIG>
F:28-60/Domain: EGF homology <EG1>
F:68-107/Domain: EGF homology <EG2>
F:110-267/Domain: discoidin I amino-terminal homology <DN1>
F:271-427/Domain: discoidin I amino-terminal homology <DN2>

Query Match 42.2%; Score 367.5; DB 2; Length 427;
Best Local Similarity 45.3%; Pred. No. 1-2e-27;
Matches 73; Conservative 28; Mismatches 57; Indels 3; Gaps 2;

QY 1 CDLNSCMPUGMSKSAISDAQITASSYFT--NMFA-TWSPSKARLHLQGSNAWRQVYN 57
Db 267 CELHGGSEPLGLKNTIPDSQITASSSYKTWNLRFQWYFHLGLDNLQCKINAWTAQSNS 326
QY 58 PREWLQVDFQTKWKVTGVTQGVKSLTSMYVKEFLISSODGHQWTLFFQNGKVVFQ 117
Db 327 AKEWLQVDFQTKVKVGIITQGARDGHQIVASYKVAHSDGQVTVVEEGTSKVFQ 386
QY 118 NQDSFTPVNLSPPPLLTRYLRIHPQSWHQAIALRMEVLGC 158
Db 387 NLDNNSHKKNIFEKPFPMARYVRVLPISWHNRITLRLELGC 427

RESULT 9
A36479
milk fat globule membrane protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A36479
R:Stubbs, J.D.; Lekutis, C.; Singer, K.L.; Bui, A.; Yuzuki, D.; Srinivasan, U.; Parry, G.
Proc. Natl. Acad. Sci. U.S.A. 87, 8417-8421, 1990
A:Title: cDNA cloning of a mouse mammary epithelial cell surface protein reveals the existence of a novel protein family.
A:Reference number: A36479; MUID:91046008; PMID:2122482
A:Accession: A36479
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-463 <STU>
A:Cross-references: DB:M38337; NID:gl99142; PIDN:AAA39534.1; PID:gi99143
C:Superfamily: milk fat globule protein; discoidin I amino-terminal homology; EGF homology
C:Keywords: membrane protein
F:28-60/Domain: EGF homology <EG1>
F:68-107/Domain: EGF homology <EG2>
F:147-303/Domain: discoidin I amino-terminal homology <DN1>
F:307-463/Domain: discoidin I amino-terminal homology <DN2>

Query Match 40.6%; Score 353.5; DB 1; Length 463;
Best Local Similarity 42.9%; Pred. No. 2.9e-26;
Matches 69; Conservative 32; Mismatches 57; Indels 3; Gaps 2;

Db 2168 NNNVRGHVQNFNPPIISPIRIIPKWTNQSIARLLEFG---DMY 2211

RESULT 8
JC4915
ags protein precursor - rat
N:Alternate names: O-acetyl-Gd3 ganglioside
C:Species: Rattus norvegicus (Norway rat)
C:Date: 26-Sep-1996 #sequence_revision 01-Nov-1996 #text_change 20-Jun-2000
C:Accession: JC4915
R:Ogura, K.; Nara, K.; Watanabe, Y.; Kohno, K.; Tai, T.; Sanai, Y.
Biochem. Biophys. Res. Commun. 225, 932-938, 1996
A:Title: Cloning and expression of cDNA for O-acetylation of GD3 ganglioside.
A:Reference number: JC4915; MUID:96374422; PMID:8780713
A:Accession: JC4915
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-427 <OGU>
A:Cross-references: DDBJ:D84068; NID:gl620006; PIDN:BA12210.1; PID:gl620007
A:Experimental source: CST cell
C:Comment: This protein is required for the O-acetylation of disialoganglioside sialic acid.
A:Genetics:
C:Superfamily: milk fat globule protein; discoidin I amino-terminal homology; EGF homology
F:1-21/Domain: signal sequence #status predicted <SIG>
F:28-60/Domain: EGF homology <EG1>
F:68-107/Domain: EGF homology <EG2>
F:110-267/Domain: discoidin I amino-terminal homology <DN1>
F:271-427/Domain: discoidin I amino-terminal homology <DN2>

Query Match 42.2%; Score 367.5; DB 2; Length 427;
Best Local Similarity 45.3%; Pred. No. 1-2e-27;
Matches 73; Conservative 28; Mismatches 57; Indels 3; Gaps 2;

QY 1 CDLNSCMPUGMSKSAISDAQITASSYFT--NMFA-TWSPSKARLHLQGSNAWRQVNN 57
Db 267 CELHGGSEPLGLKNTIPDSQITASSSYKTWNLRFQWYFHLGLDNLQGNKINAWTAQSNS 326
QY 58 PREWLQVDFQTKWKVTGVTQGVKSLTSMYVKEFLISSODGHQWTLFFQNGKVVFQ 117
Db 327 AKEWLQVDFQTKVTCITQGARDGHQIVASYKVAHSDGQVTVVEEGTSTVFQ 386
QY 118 NQDSFTPVNLSPPPLTRYLRHPOSWVHQAIRMEVLGC 158
Db 387 NLDNNSHKKNIFEKPFPMARYVRVLPISWNNRITLRLELGC 427

RESULT 9
A36479
milk fat globule membrane protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A36479
R:Stubbs, J.D.; Lekutis, C.; Singer, K.L.; Bui, A.; Yuzuki, D.; Srinivasan, U.; Parry, G.
Proc. Natl. Acad. Sci. U.S.A. 87, 8417-8421, 1990
A:Title: cDNA cloning of a mouse mammary epithelial cell surface protein reveals the existence of a novel protein family.
A:Reference number: A36479; MUID:91046008; PMID:2122482
A:Accession: A36479
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-463 <STU>
A:Cross-references: DB:M38337; NID:gl99142; PIDN:AAA39534.1; PID:gi99143
C:Superfamily: milk fat globule protein; discoidin I amino-terminal homology; EGF homology
C:Keywords: membrane protein
F:28-60/Domain: EGF homology <EG1>
F:68-107/Domain: EGF homology <EG2>
F:147-303/Domain: discoidin I amino-terminal homology <DN1>
F:307-463/Domain: discoidin I amino-terminal homology <DN2>

Query Match 40.6%; Score 353.5; DB 1; Length 463;
Best Local Similarity 42.9%; Pred. No. 2.9e-26;
Matches 69; Conservative 32; Mismatches 57; Indels 3; Gaps 2;

Job time : 16 secs

Query Match	30.1%;	Score 262;	DB 2;	Length 845;
Best Local Similarity	33.1%;	Pred. No. 4.2e-17;		
Matches	54;	Conservative	32;	Mismatches 67; Indels 10; Gaps 2;

QY	9	P	C	M	E	S	K	A	I	S	D	A	O	I	T	A	S	S	F	I	N	F	M	F	A	T	S	P	S	X	A	R	L	H	G	O	R	S	-----	N	A	M	P	O	V	N	N	K	E	W	61		
DB	74	P	G	M	E	S	H	R	I	E	D	I	O	I	A	S	S	M	L	H	G	L	C	A	---	O	Q	R	L	N	M	O	T	G	A	T	E	D	D	Y	O	G	A	C	A	E	D	D	A	T	O	W	130
QY	62	L	O	V	D	F	O	K	M	K	V	T	G	T	O	G	V	K	S	L	L	T	S	M	Y	K	E	L	I	S	S	O	D	G	H	O	W	T	F	F	O	G	K	V	K	V	Q	N	O	D	S	121	
DB	131	I	E	V	D	R	T	R	T	F	G	V	T	O	C	R	D	S	I	H	D	F	V	T	T	F	F	G	S	N	D	S	O	T	M	N	W	T	Y	G	E	M	T	F	H	G	N	V	D	K	190		
QY	122	F	T	P	V	N	S	L	D	P	P	L	T	R	A	I	H	P	O	S	M	V	H	O	A	L	M	E	V	L	G	E	A	O	D	L	Y	164															
DB	191	D	R	P	V	S	E	L	P	E	P	V	A	F	I	P	T	M	N	G	S	L	C	M	E	V	L	G	S	V	A	P	V	233																			

RESULT 15

Q00948
A5 antigen precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: JH0456; JQ0948
R: Takagi, S.; Hirata, T.; Agata, K.; Mochii, M.; Eguchi, G.; Fujisawa, H.
Neuron 7, 295-307, 1991
A:Title: The A5 antigen, a candidate for the neuronal recognition molecule, has homology
A:Reference number: JH0466; MUID:51337458; PMID:1908252
A:Accession: JH0466
A:Molecule type: mRNA
A:Residues: 1-927 <RAK>
A:Cross-references: GB:10467; GB:D01077; NID:G222962; PIDN:BAA01260.1;PID:G222963

A;Experimental source: Leupold, Brian
A;Note: This protein has motifs homologous to complement components C1r and C1s and to C1r1
C;Comment: This protein is a neuronal cell surface molecule involved in the neuronal repair
C;Superfamily: Xenopus A5 antigen; C1r/C1s repeat homology; discoidin I amino-terminal R
C;Keywords: duplication; glycoprotein; transmembrane protein
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-927/Product: A5 antigen #status predicted <ASA>
F;27-138/Domain: C1r/C1s repeat homology <C1R1>
F;147-262/Domain: C1r/C1s repeat homology <C1R2>
F;274-424/Domain: discoidin I amino-terminal homology <DN1>
F;430-584/Domain: discoidin I amino-terminal homology <DN2>
F;646-812/Domain: MAM homology <MAM>
F;861-883/Domain: transmembrane #status predicted <TM>
F;150-261-300-523-844/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	29.2%	Score 254.5;	DB 1;	Length 927;
Best Local Similarity	34.6%	Pred. No. 2.5e-16;		
Matches 55:	Conservative	26;	Mismatches 71;	Indels 7; Gaps 3;

Qy	6	CSMPLGWESKALISDAQITASSYFTNMFTATWSKAEHLQGRSNARVQVNNPKENLOVD	65
Db	275	CKBALGWESGEIHFDQISVSSQYS---NMWSAERLKNV--ENGWTPGEVTVKVENLOVD	329
Qy	66	FQTKMKVTVGTTQGV--KSLLSMYVKEFLISSODGHQWTLFFGNGKVKVQGNQDSFT	123
Db	330	LENLRFVSGHGTGGAISKETKKYFVKYSKVDSINGEDWITLKDGNKHLFTGNTDATD	389
Qy	124	PVNSLDPPLLTRYLRHPQSWVHQIALRMEVLGCEAD	162
Db	390	VYWRPTSKPITFVRLRPVTVWENGISLRFELYGCKITD	428

Search completed: September 29, 2004, 16:40:24

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 29, 2004, 16:38:04 ; Search time 33 Seconds
(without alignments)
256.565 Million cell updates/sec

Title: US-10-049-399a-1_COPY_2169_2332
Perfect score: 871
Sequence: 1 CDLNSCSPLGMSKAISSDA.....WVHQIALRMEVLGCEAQLDLY 164

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/2/iaa/5A COMB.pcp.*
- 2: /cgn2_6/prodata/2/iaa/5B COMB.pcp.*
- 3: /cgn2_6/prodata/2/iaa/6A COMB.pcp.*
- 4: /cgn2_6/prodata/2/iaa/6B COMB.pcp.*
- 5: /cgn2_6/prodata/2/iaa/PCITUS COMB.pcp.*
- 6: /cgn2_6/prodata/2/iaa/backfile1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	871	100.0	1438	4	US-09-209-916-1
2	871	100.0	1471	1	US-08-683-839B-3
3	871	100.0	1661	2	US-08-882-083-2
4	871	100.0	1661	2	US-08-558-107-2
5	871	100.0	1661	3	US-09-243-539-2
6	871	100.0	2332	1	US-07-864-004B-4
7	871	100.0	2332	1	US-08-251-937A-4
8	871	100.0	2332	1	US-08-212-133A-2
9	871	100.0	2332	1	US-08-276-594A-2
10	871	100.0	2332	1	US-08-474-503-2
11	871	100.0	2332	2	US-08-670-707A-2
12	871	100.0	2332	3	US-09-037-601-2
13	871	100.0	2332	3	US-09-324-867-3
14	871	100.0	2332	4	US-09-315-179-2
15	871	100.0	2332	4	US-09-523-656-2
16	871	100.0	2332	5	PCT-US93-03275-4
17	871	100.0	2332	5	PCT-US94-13200-2
18	871	100.0	2351	1	US-08-121-202-2
19	871	100.0	2351	1	US-08-366-851A-2
20	871	100.0	2351	4	US-10-133-907-4
21	871	100.0	2351	6	5171844-2
22	867	99.5	218	1	US-07-607-538C-5
23	867	99.5	218	2	US-08-162-402B-5
24	867	99.5	218	4	US-09-364-185-5
25	862	99.0	2351	6	5422260-1
26	846	97.1	160	2	US-08-162-402B-15
27	846	97.1	160	4	US-09-331-793-9

28	752	86.3	2304	3	US-09-324-867-4	Sequence 4, Appli
29	752	86.3	2319	1	US-08-212-133A-8	Sequence 8, Appli
30	752	86.3	2319	1	US-08-474-503-6	Sequence 6, Appli
31	752	86.3	2319	2	US-08-670-707A-6	Sequence 6, Appli
32	752	86.3	2319	3	US-09-037-601-6	Sequence 6, Appli
33	752	86.3	2319	4	US-09-315-179-6	Sequence 28, Appli
34	752	86.3	2319	4	US-09-523-656-28	Sequence 6, Appli
35	752	86.3	2319	5	PCT-US94-13200-6	Sequence 2, Appli
36	736	84.5	2343	3	US-09-324-867-2	Sequence 39, Appli
37	720	82.7	1443	2	US-08-670-707A-39	Sequence 39, Appli
38	720	82.7	1443	3	US-09-037-601-39	Sequence 39, Appli
39	720	82.7	1443	4	US-09-315-179-39	Sequence 38, Appli
40	720	82.7	1467	4	US-09-523-656-38	Sequence 5, Appli
41	720	82.7	2115	3	US-09-324-867-5	Sequence 37, Appli
42	720	82.7	2133	2	US-08-670-707A-37	Sequence 37, Appli
43	720	82.7	2133	3	US-09-037-601-37	Sequence 37, Appli
44	720	82.7	2133	4	US-09-315-179-37	Sequence 30, Appli
45	720	82.7	2133	4	US-09-523-656-30	

ALIGNMENTS

RESULT 1
US-09-209-916-1
; Sequence 1, Application US/09209916
; Patent No. 6358703
; GENERAL INFORMATION:
; APPLICANT: Cho, Myung-Sam
; APPLICANT: Chan, Sham-Yuen
; APPLICANT: Kelsey, William
; APPLICANT: Yee, Helena
; TITLE OF INVENTION: Expression System for Factor VIII
; FILE REFERENCE: MSB-7255
; CURRENT APPLICATION NUMBER: US/09/209,916
; CURRENT FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1438
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Derived from
; OTHER INFORMATION: human factor VIII sequence
US-09-209-916-1

Query Match	100.0%	Score	871	DB	4	Length	1438
Best Local Similarity	100.0%	Pred. No.	4e-94				
Matches	164	Conservative	0	Mismatches	0	Indels	0
Gaps	0						
QY	1	CDLNSCSPLGMSKAISSDAQITASSYFTNNFATWSPSKARHLHOGSNMRPQVNNPKE	60				
Db	1275	CDLNSCSPLGMSKAISSDAQITASSYFTNNFATWSPSKARHLHOGSNMRPQVNNPKE	1334				
QY	61	WLQVDFQKTMKVTGTTQGVKSLTSMYVKEFLISSSDQGHQWTLFFQNGKVKVFGNQD	120				
Db	1335	WLQVDFQKTMKVTGTTQGVKSLTSMYVKEFLISSSDQGHQWTLFFQNGKVKVFGNQD	1394				
QY	121	SFTPVVNSLDPPLLRYLRHPQSWHQAIALRMEVLGCEAQLDLY	164				
Db	1395	SFTPVVNSLDPPLLRYLRHPQSWHQAIALRMEVLGCEAQLDLY	1438				

RESULT 2
US-08-683-839B-3
; Sequence 3, Application US/08683839B
; Patent No. 5744326
; GENERAL INFORMATION:
; APPLICANT: Iill, Charles . R. et al.
; TITLE OF INVENTION: Use of Viral Cis-Acting Post-Transcriptional
; TITLE OF INVENTION: Regulatory Sequences To Increase Expression of
; TITLE OF INVENTION: Introns Genes Containing Near-Consensus Splice Sites

```

;
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/683,839B
; FILING DATE: 11-MARCH-1996
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; NAME: Remillard, Jane B.
; REGISTRATION NUMBER: 38,872
; REFERENCE/DOCKET NUMBER: TTI-138
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1471 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-683-839B-3

Query Match 100.0%; Score 871; DB 1; Length 1471;
Best Local Similarity 100.0%; Pred. No. 4.1e-94;
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDLNSCMPGLGMSKAIISDAQITASSYFTNMFTWSPSKARLHLOGRSNAWRPQVNNPKE 60
DB 1308 CDLNSCMPGLGMSKAIISDAQITASSYFTNMFTWSPSKARLHLOGRSNAWRPQVNNPKE 1367
QY 61 WLQVDFQKTKMKTGVTGQVKSLTSMYKKEFLISSQDGHQWTLFFQNGKVKVFGNQD 120
DB 1368 WLQVDFQKTKMKTGVTGQVKSLTSMYKKEFLISSQDGHQWTLFFQNGKVKVFGNQD 1427
QY 121 SFTPVVNSLDPPLLTRYLRIHPQSWHQAIRMEVLGCEAQDLY 164
DB 1428 SFTPVVNSLDPPLLTRYLRIHPQSWHQAIRMEVLGCEAQDLY 1471

RESULT 3
US-08-682-083-2
; Sequence 2, Application US/08882083
; Patent No. 5869292
; GENERAL INFORMATION:
; APPLICANT: VOORBERG, Johannes J.
; TITLE OF INVENTION: HYBRID PROTEINS WITH MODIFIED ACTIVITY
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: ISACSON, John P.
; REGISTRATION NUMBER: 33,715
; REFERENCE/DOCKET NUMBER: 30472/212
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1661 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-882-083-2

Query Match 100.0%; Score 871; DB 2; Length 1661;
Best Local Similarity 100.0%; Pred. No. 4.9e-94;
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDLNSCMPGLGMSKAIISDAQITASSYFTNMFTWSPSKARLHLOGRSNAWRPQVNNPKE 60
DB 1498 CDLNSCMPGLGMSKAIISDAQITASSYFTNMFTWSPSKARLHLOGRSNAWRPQVNNPKE 1557
QY 61 WLQVDFQKTKMKTGVTGQVKSLTSMYKKEFLISSQDGHQWTLFFQNGKVKVFGNQD 120
DB 1558 WLQVDFQKTKMKTGVTGQVKSLTSMYKKEFLISSQDGHQWTLFFQNGKVKVFGNQD 1617
QY 121 SFTPVVNSLDPPLLTRYLRIHPQSWHQAIRMEVLGCEAQDLY 164
DB 1618 SFTPVVNSLDPPLLTRYLRIHPQSWHQAIRMEVLGCEAQDLY 1661

RESULT 4
US-08-558-107-2
; Sequence 2, Application US/08558107
; Patent No. 5910481
; GENERAL INFORMATION:
; APPLICANT: VOORBERG, Johannes J.
; TITLE OF INVENTION: HYBRID PROTEINS WITH MODIFIED ACTIVITY
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/558,107
; FILING DATE: 13-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: ISACSON, John P.
; REGISTRATION NUMBER: 33,715
; REFERENCE/DOCKET NUMBER: 30472/212
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1661 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-882-083-2
```

LENGTH: 1661 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-558-107-2

Query Match 100.0%; Score 871; DB 2; Length 1661;
Best Local Similarity 100.0%; Pred. No. 4.9e-94;
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDLNSCSMPLGWESKAISDAQITASSYFTNMFAWSPSKARLHLQGRSNARWPQVNNPKE 60
DB 1498 CDLNSCSMPLGWESKAISDAQITASSYFTNMFAWSPSKARLHLQGRSNARWPQVNNPKE 1557
QY 61 WLQVDFQKTMKVTGVTTCQVKSLLTSMYKFEFLISSQDGHQWTLFFQNGKVKVFQGNQD 120
DB 1558 WLQVDFQKTMKVTGVTTCQVKSLLTSMYKFEFLISSQDGHQWTLFFQNGKVKVFQGNQD 1617
QY 121 SFTPVVNSLDPPLRLRYLRHQPQSWHQAIALRMEVLGCEAODLY 164
DB 1618 SFTPVVNSLDPPLRLRYLRHQPQSWHQAIALRMEVLGCEAODLY 1661

RESULT 5

US-09-243-539-2
; Sequence 2, Application US/09243539
; Patent No. 6130203
; GENERAL INFORMATION:
; APPLICANT: VOORBERG, Johannes J.
; TITLE OF INVENTION: HYBRID PROTEINS WITH MODIFIED ACTIVITY
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/243,539
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/558,107
; FILING DATE: 13-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: ISACSON, John P.
; REGISTRATION NUMBER: 33,715
; REFERENCE/DOCKET NUMBER: 30472/212
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1661 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-243-539-2

Query Match 100.0%; Score 871; DB 3; Length 1661;
Best Local Similarity 100.0%; Pred. No. 4.9e-94;
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDLNSCSMPLGWESKAISDAQITASSYFTNMFAWSPSKARLHLQGRSNARWPQVNNPKE 60
DB 1498 CDLNSCSMPLGWESKAISDAQITASSYFTNMFAWSPSKARLHLQGRSNARWPQVNNPKE 1557

QY 61 WLQVDFQKTMKVTGVTTCQVKSLLTSMYKFEFLISSQDGHQWTLFFQNGKVKVFQGNQD 120
DB 1558 WLQVDFQKTMKVTGVTTCQVKSLLTSMYKFEFLISSQDGHQWTLFFQNGKVKVFQGNQD 1617
QY 121 SFTPVVNSLDPPLRLRYLRHQPQSWHQAIALRMEVLGCEAODLY 164
DB 1618 SFTPVVNSLDPPLRLRYLRHQPQSWHQAIALRMEVLGCEAODLY 1661

RESULT 6

US-07-864-004B-4
; Sequence 4, Application US/07864004B
; Patent No. 5364771
; GENERAL INFORMATION:
; APPLICANT: Lollar, John S.
; TITLE OF INVENTION: Hybrid Human/Porcine Factor VIII
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kilpatrick & Cody
; STREET: 1100 Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: US
; ZIP: 30309
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/864,004B
; FILING DATE: 07 APRIL 1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: EMU106
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-815-6508
; TELEFAX: 404-815-6555
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2332 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapien
; TISSUE TYPE: Liver CDNA sequence
US-07-864-004B-4

Query Match 100.0%; Score 871; DB 1; Length 2332;
Best Local Similarity 100.0%; Pred. No. 8.2e-94;
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDLNSCSMPLGWESKAISDAQITASSYFTNMFAWSPSKARLHLQGRSNARWPQVNNPKE 60
DB 2169 CDLNSCSMPLGWESKAISDAQITASSYFTNMFAWSPSKARLHLQGRSNARWPQVNNPKE 2228
QY 61 WLQVDFQKTMKVTGVTTCQVKSLLTSMYKFEFLISSQDGHQWTLFFQNGKVKVFQGNQD 120
DB 2229 WLQVDFQKTMKVTGVTTCQVKSLLTSMYKFEFLISSQDGHQWTLFFQNGKVKVFQGNQD 2288
QY 121 SFTPVVNSLDPPLRLRYLRHQPQSWHQAIALRMEVLGCEAODLY 164
DB 2289 SFTPVVNSLDPPLRLRYLRHQPQSWHQAIALRMEVLGCEAODLY 2332

RESULT 7
 US-08-251-937A-4
 ; Sequence 4, Application US/08251937A
 ; Patent No. 5583209
 ; GENERAL INFORMATION:
 ; APPLICANT: Lollar, John S.
 ; APPLICANT: Runge, Marshall S.
 ; TITLE OF INVENTION: Hybrid Human/Porcine Factor VIII
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Kilpatrick & Cody
 ; STREET: 1100 Peachtree Street
 ; CITY: Atlanta
 ; STATE: Georgia
 ; COUNTRY: US
 ; ZIP: 30309
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/251,937A
 ; FILING DATE: 31-MAY-1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/864,004
 ; FILING DATE: 07-APR-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Pratt, John S.
 ; REGISTRATION NUMBER: 29,476
 ; REFERENCE/DOCKET NUMBER: EMU106DIV
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 404-815-6367
 ; TELEFAX: 404-815-6555
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2332 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: N-terminal
 ; ORIGINAL SOURCE:
 ; ORGANISM: Homo sapien
 ; TISSUE TYPE: Liver cdna sequence
 ; US-08-251-937A-4

Query Match 100.0%; Score 871; DB 1; Length 2332;
 Best Local Similarity 100.0%; Pred. No. 8.2e-94;
 Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CDLNSCSMPGLMESKAISDAQITASSYFTNMFATWSPSKARHLQGRSNARPPQVNNPKE 60
 DB 2169 CDLNSCSMPGLMESKAISDAQITASSYFTNMFATWSPSKARHLQGRSNARPPQVNNPKE 2228
 QY 61 WLQVDFQKTKMKTGVTTQGVKSLTSMYKVELISSQDGHQWTLFFQNGKVKVFGNQD 120
 DB 2229 WLQVDFQKTKMKTGVTTQGVKSLTSMYKVELISSQDGHQWTLFFQNGKVKVFGNQD 2288
 QY 121 SFTPVVNSLDPPLLTLYLRIHQSWWHQIALRMEVLGCEAQDLY 164
 DB 2289 SFTPVVNSLDPPLLTLYLRIHQSWWHQIALRMEVLGCEAQDLY 2332

RESULT 8
 US-08-212-133A-2
 ; Sequence 2, Application US/08212133A
 ; Patent No. 5663060
 ; GENERAL INFORMATION:
 ; APPLICANT: YONEMURA, Hiroshi
 ; APPLICANT: TAJIMA, Yoshitaka
 ; APPLICANT: SUGAWARA, Kenishin
 ; APPLICANT: MASUDA, Kenichi
 ; TITLE OF INVENTION: PROCESS FOR PREPARING HUMAN COAGULATION
 ; FACTOR VIII PROTEIN COMPLEX

; APPLICANT: Lollar, John S.
 ; APPLICANT: Runge, Marshall S.
 ; TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Kilpatrick & Cody
 ; STREET: 100 Peachtree Street
 ; CITY: Atlanta
 ; STATE: Georgia
 ; COUNTRY: US
 ; ZIP: 30303
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/212,133A
 ; FILING DATE: March 11, 1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/864,004
 ; FILING DATE: 07-APR-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Pabst, Patrea L.
 ; REGISTRATION NUMBER: 31,284
 ; REFERENCE/DOCKET NUMBER: EMU/76677
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 404-572-6508
 ; TELEFAX: 404-572-6555
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2332 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: YES
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: N-terminal
 ; ORIGINAL SOURCE:
 ; ORGANISM: Homo sapien
 ; TISSUE TYPE: Liver cdna sequence
 ; US-08-212-133A-2
 Query Match 100.0%; Score 871; DB 1; Length 2332;
 Best Local Similarity 100.0%; Pred. No. 8.2e-94;
 Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CDLNSCSMPGLMESKAISDAQITASSYFTNMFATWSPSKARHLQGRSNARPPQVNNPKE 60
 DB 2169 CDLNSCSMPGLMESKAISDAQITASSYFTNMFATWSPSKARHLQGRSNARPPQVNNPKE 2228
 QY 61 WLQVDFQKTKMKTGVTTQGVKSLTSMYKVELISSQDGHQWTLFFQNGKVKVFGNQD 120
 DB 2229 WLQVDFQKTKMKTGVTTQGVKSLTSMYKVELISSQDGHQWTLFFQNGKVKVFGNQD 2288
 QY 121 SFTPVVNSLDPPLLTLYLRIHQSWWHQIALRMEVLGCEAQDLY 164
 DB 2289 SFTPVVNSLDPPLLTLYLRIHQSWWHQIALRMEVLGCEAQDLY 2332
 RESULT 9
 US-08-276-594A-2
 ; Sequence 2, Application US/08276594A
 ; Patent No. 5693499
 ; GENERAL INFORMATION:
 ; APPLICANT: YONEMURA, Hiroshi
 ; APPLICANT: TAJIMA, Yoshitaka
 ; APPLICANT: SUGAWARA, Kenishin
 ; APPLICANT: MASUDA, Kenichi
 ; TITLE OF INVENTION: PROCESS FOR PREPARING HUMAN COAGULATION
 ; FACTOR VIII PROTEIN COMPLEX


```
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/212,133
/ FILING DATE: 11-MAR-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/864,004
/ FILING DATE: 07-APR-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Greenlee, Lorraine L.
/ REGISTRATION NUMBER: 27,894
/ REFERENCE/DOCKET NUMBER: 75-95F
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 303/499-8080
/ TELEFAX: 303/499-8089
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2332 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: not relevant
/ MOLECULE TYPE: protein
/ HYPOTHEICAL: YES
/ ANTI-SENSE: NO
/ FRAGMENT TYPE: N-terminal
/ ORIGINAL SOURCE:
/ ORGANISM: Homo sapiens
/ TISSUE TYPE: Liver
/ US-08-670-707A-2

Query Match 100.0%; Score 871; DB 2; Length 2332;
Best Local Similarity 100.0%; Pred. No. 8.2e-94;
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDLNSCMPGMSKALSDAQITASSYFTNMFWATWSPSKARLHLOGRSNARFPQVNNPKE 60
Db 2169 CDLNSCMPGMSKALSDAQITASSYFTNMFWATWSPSKARLHLOGRSNARFPQVNNPKE 2228

QY 61 WLQVDFQKTKVGTGTQGVKSLTSMYKVEFLISSQDGHQWTLFFQNGKVKVFGNQD 120
Db 2229 WLQVDFQKTKVGTGTQGVKSLTSMYKVEFLISSQDGHQWTLFFQNGKVKVFGNQD 2288

QY 121 SFTPVNSLDPPLLTRYLRHPSQSWHQIALRMEVLGCEAQDLY 164
Db 2289 SFTPVNSLDPPLLTRYLRHPSQSWHQIALRMEVLGCEAQDLY 2332

RESULT 12
US-09-037-601-2
; Sequence 2, Application US/09037601
; Patent No. 6180371
; GENERAL INFORMATION:
; APPLICANT: Lollar, John S.
; TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle Suite 201
; CITY: Boulder
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/037,601
; FILING DATE: 26-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US94/13200
; FILING DATE: 15-NOV-1994
; PRIOR APPLICATION DATA:
```

```
/
/ APPLICATION NUMBER: US 08/212,133
/ FILING DATE: 11-MAR-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/864,004
/ FILING DATE: 07-APR-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Ferber, Donna M.
/ REGISTRATION NUMBER: 33,878
/ REFERENCE/DOCKET NUMBER: 75-95F
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 303/499-8080
/ TELEFAX: 303/499-8089
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2332 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: not relevant
/ MOLECULE TYPE: protein
/ HYPOTHEICAL: YES
/ ANTI-SENSE: NO
/ FRAGMENT TYPE: N-terminal
/ ORIGINAL SOURCE:
/ ORGANISM: Homo sapiens
/ TISSUE TYPE: Liver
/ US-09-037-601-2

Query Match 100.0%; Score 871; DB 3; Length 2332;
Best Local Similarity 100.0%; Pred. No. 8.2e-94;
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDLNSCMPGMSKALSDAQITASSYFTNMFWATWSPSKARLHLOGRSNARFPQVNNPKE 60
Db 2169 CDLNSCMPGMSKALSDAQITASSYFTNMFWATWSPSKARLHLOGRSNARFPQVNNPKE 2228

QY 61 WLQVDFQKTKVGTGTQGVKSLTSMYKVEFLISSQDGHQWTLFFQNGKVKVFGNQD 120
Db 2229 WLQVDFQKTKVGTGTQGVKSLTSMYKVEFLISSQDGHQWTLFFQNGKVKVFGNQD 2288

QY 121 SFTPVNSLDPPLLTRYLRHPSQSWHQIALRMEVLGCEAQDLY 164
Db 2289 SFTPVNSLDPPLLTRYLRHPSQSWHQIALRMEVLGCEAQDLY 2332

RESULT 13
US-09-324-867-3
; Sequence 3, Application US/09324867A
; Patent No. 6251632
; GENERAL INFORMATION:
; APPLICANT: Lillcrap, David
; APPLICANT: Cameron, Cherie
; TITLE OF INVENTION: Hydril Human/Animal Factor VIII
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Horrocks, L. Suzanne Hoyle
; STREET: 5370 Manhattan Circle Suite 201
; CITY: Boulder
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/324,867A
; FILING DATE: 26-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US94/13200
; FILING DATE: 15-NOV-1994
; PRIOR APPLICATION DATA:
```


Qy		1	CDJNSCMPLGMSKAISDAQITASSYFTKNFATWSPSKARLHLQGSNAWRPQVNNPK	E60
Dbb		2169	CDJNSCMPLGMSKAISDAQITASSYFTKNFATWSPSKARLHLQGSNAWRPQVNNPK	2228
Qy		61	WLQVDFOKTMKVGTVTQQGVKSLLTSMYVKXEFLISSSDGQHMTLPFGNGKKVFQGNQD	120
Dbb		2229	WLQVDFOKTMKVGTVTQQGVKSLLTSMYVKXEFLISSSDGQHMTLPFGNGKKVFQGNQD	2288
Qy		121	SFTPEVNLSDDPLLTRYLRTHPOSWHQIALRMEVLGCEAQDLV	164
Dbb		2289	SFTPEVNLSDDPLLTRYLRTHPOSWHQIALRMEVLGCEAQDLV	2332

RESULT 14

```

US-09-315-179-2
; Sequence 2, Application US/09315179
; Patent No. 6376463
; GENERAL INFORMATION:
; APPLICANT: Lollar, John S
; TITLE OF INVENTION: Modified Factor VIII
; FILE REFERENCE: 75-95H
; CURRENT APPLICATION NUMBER: US/09/315,179
; CURRENT FILING DATE: 1999-05-20
; EARLIER APPLICATION NUMBER: U.S. 09/037,601
; EARLIER FILING DATE: 1998-03-10
; EARLIER APPLICATION NUMBER: U.S. 08/670,707
; EARLIER FILING DATE: 1996-06-26
; EARLIER APPLICATION NUMBER: PCT/US97/11155
; EARLIER FILING DATE: 1997-06-26
; EARLIER APPLICATION NUMBER: PCT/US94/13200
; EARLIER FILING DATE: 1994-11-15
; EARLIER APPLICATION NUMBER: U.S. 08/212,133
; EARLIER FILING DATE: 1994-03-11
; EARLIER APPLICATION NUMBER: U.S. 07/864,004
; EARLIER FILING DATE: 1992-04-07
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2332
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-315-179-2

```

Query Match	100.0%;	Score 871;	DB 4;	Length 2332;
Best Local Similarity	100.0%;	Pred. No. 8.2e-94;		
Matches 164;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY 1	CDLNSCSPLGMESKAISDAQITASSYFTWNEFATWSPSKARLHLOGSNARWQVNNPKX	60		
Db 2169	CDLNSCSPLGMESKAISDAQITASSYFTWNEFATWSPSKARLHLOGSNARWQVNNPKX	2228		
QY 61	WLQVDFQKMKVGTGVTQTQGVKSLTSMYVKEFLISSQDGHQWTLFPQGNKVVFQGNQD	120		
Db 2229	WLQVDFQKMKVGTGVTQTQGVKSLTSMYVKEFLISSQDGHQWTLFPQGNKVVFQGNQD	2288		
QY 121	SFTFVNVNSLDPPLLTLYRLRHPSQSWHQIALRNEVLGCEAQDLY	164		
Db 2289	SFTFVNVNSLDPPLLTLYRLRHPSQSWHQIALRNEVLGCEAQDLY	2332		

RESULT 15

```

US09-523-656-2
; Sequence 2, Application US/09523656
; Patent No. 6458563
; GENERAL INFORMATION:
; APPLICANT: Lollar S., John
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: 75-951
; CURRENT APPLICATION NUMBER: US/09/523,656
; CURRENT FILING DATE: 2000-03-10
; EARLIER APPLICATION NUMBER: 09/037,601
; EARLIER FILING DATE: 1998-03-10

```

This Page Blank (uspto)